

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 12.0425 Seconds
(without alignments)
1509.673 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDSVYVSMLEPLTATQAN.....GLOASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Piri.*
2: Piri2.*
3: Piri3.*
4: Piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	2	I59421
2	201	19.6	225	2	I38700
3	193	18.9	257	2	I50146
4	191	18.7	227	2	A46467
5	190	18.6	233	2	P70372
6	182	17.8	231	2	P70374
7	180	17.6	216	2	P70375
8	178.5	17.4	240	2	I54524
9	176	17.2	404	2	A46274
10	175.5	17.2	223	2	A35917
11	174.5	17.1	304	2	JX0209
12	174	17.0	199	2	JH0822
13	169	16.5	237	2	JH7608
14	167	16.3	301	2	S13165
15	166	16.2	156	2	T28141
16	165	16.1	284	2	S29855
17	164.5	16.1	306	2	A42230
18	162	15.8	262	2	A30573
19	162	15.8	262	2	A45813
20	160.5	15.7	223	2	B46467
21	160.5	15.7	284	1	LNRT1
22	160.5	15.7	301	1	LNRT2
23	157.5	15.4	291	1	LNHUL
24	157	15.3	262	2	I49361
25	156	15.2	1487	2	S48719
26	153.5	15.0	167	1	WVZF2
27	151.5	14.8	260	2	I49049
28	149	14.6	170	2	T28140
29	148.5	14.5	220	2	C46467

30	148.5	14.5	550	2	A28166	Kupffer cell recep
31	146.5	14.3	1326	2	B56395	secretory phosphol
32	146.5	14.3	1465	2	A56395	secretory phosphol
33	146	14.3	311	1	LNHU2A	asialoglycoprotein
34	145.5	14.2	1479	2	T42710	mannose receptor,
35	143.5	14.0	144	2	PC7027	aggratin alpha cha
36	142	13.9	146	2	JC7135	agkissacutacin beta
37	141.5	13.8	1458	1	A49707	phospholipase A2 r
38	140.5	13.7	267	2	I49053	ly-49G.2 antigen -
39	140.5	13.7	280	2	I49052	chondroitin sulfat
40	139.5	13.6	3562	2	A47171	phospholipase A2 r
41	138.5	13.5	1463	2	A53210	pancreatitis-assoc
42	137.5	13.4	175	2	S29822	pancreatic stone p
43	137	13.4	165	2	A28351	natural killer cel
44	137	13.4	286	2	I49363	scavenger receptor
45	137	13.4	742	2	JC7595	

ALIGNMENTS

RESULT 1
I59421

mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C/Accession: I59421

R;Guthmann, M.D.; Tal, M.; Pecht, I.

Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995

A>Title: A secretion inhibitory signal transduction molecule on mast cells is another C

A:Reference number: I59421; MUID:96016176; PMID:7568140

A:Accession: I59421

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-188 <RES>

A/Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142

C:Genetics:

A:Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 4.8e-42;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy	1	MTDSVYVSMLEPLTATQANDYGPQOKSSSKSCICVAITGLLTAVLLSVLLYQWIL	60
Db	1	MAUNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVVVALGLLTVILMSLLLYQETL	60
Qy	61	COGSNYSTCASCPDRWMKYGNHCYFFSVEEKDWNSSLEFFCLARDSHLLVITDNQEMS	120
Db	61	CCGSKGFMQCQSCRCPNLWENGSHCYFFSWEKEDWNSSLKFCADKGSLLTFFPDQGVN	120
Qy	121	LLQVFLSEATCWIGLRNNSWRWEDGSLNPSRISNSFVQTCAINKNGLOASCEVPL	180
Db	121	LFQYVGDEFYWIGLRDIDGWRWEDGPAISLS-ILSNSVVKCGTIHRCGLHASSCEVAL	179
Qy	181	HGVCKV	187
Db	180	QWICEK	186

RESULT 2

I38700

hNKR-Pla protein - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C/Accession: I38700

R;Lanier, L.L.; Chang, C.; Phillips, J.H.

J. Immunol. 153, 2417-2428, 1994

A>Title: Human NKR-PIA: A disulfide-linked homodimer of the C-type lectin superfamily

A:Reference number: I38700; MUID:94358407; PMID:8077657

A:Accession: I38700

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-225 <RES>
A;Cross-references: EMBL:U11276; NID:G538270; PIDN:AAA21605.1; PID:G544496
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 19.6%; Score 201; DB 2; Length 225;
Best Local Similarity 26.0%; Pred. No. 1.7e-11;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDSVIYSMLELPTATQAQNDYGPQKSSSKP-----SCSCLVAITLG 44
Db 1 MQQAIYAEINLPT-----DSGPSSSPSLRDVCOQSPWHQFALKLSGAGIILLVL- 53
QY 45 LITAVLLSVLLYQWILCOGSNYSTCA-----SCPSCDRWMKYGNHCYFYS 90
Db 54 VVTGLSVSYT---SLIQKSSIEKCSVDIQSQSNKKTTPRGLNCPFIYMQQLREKLLFS 109
QY 91 VEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
Db 110 HTVNPWNNSLADCSLKESLLIRDKDELIHTQNLIRDKAILFWIGLNFSLSEKNKWWIN 169
QY 146 GSPLNFS--RISSNFPVPCGAINKNGLOASCEVPLHGVCCK 186
Db 170 GSFLNSDLIRGDAKENSICISQTSVYSEYCESTEIRWICOK 212

RESULT 3
150146
gene 17.5 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50146
R;Bernot, A.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 221-229, 1994
A;Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
A;Reference number: I50146; MUID:94164691; PMID:8119728
A;Accession: I50146
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-257 <BER>
A;Cross-references: GB:M89072; NID:G505324; PIDN:AAA48558.1; PID:G505325
C;Superfamily: C-type lectin homology
F;129-241/Domain: C-type lectin homology <LCH>

Query Match 18.9%; Score 193; DB 2; Length 257;
Best Local Similarity 26.6%; Pred. No. 1.1e-10;
Matches 49; Conservative 28; Mismatches 89; Indels 18; Gaps 4;

QY 17 QAQNDYGPQKSSSKPSCSCL-----VAITGLLTAVLLSVLLYQWILCOGSNYSTC 69
Db 64 EATTREGDEERQSGRGSGSELRQNRRLVCLVALSAVPCMLVLAIVLVLRPS---C 119
QY 70 ASCPS---CPDRWMKYGNHCYFVSVEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVF 125
Db 120 SPRPFVSHVCNANWVGFOCKYIFSDTSWNSSREHCHRLGASLATIDTKEEFMLQY 179
QY 126 LSEAFPCWIGLRNNSG---WRWEDGSPNFSNFSFVQTCGAINKNGLOASCEVPLHG 182
Db 180 QRPADRWIGLHRAEGDEHTWADGSAFTNRPVFLRGGRCAYLNGDGISSALCHSEKFW 239
QY 183 VCKK 186
Db 240 VCSR 243

RESULT 4
A46467
natural killer cell receptor P1 - mouse
N;Alternate names: NKR-P1 protein
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C;Accession: A46467; A46502; A46456
R;Giorda, R.; Trucco, M.

J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated ki
A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: A46467
A;Molecule type: mRNA
A;Residues: 'MHLLCT', 1-227 <GIO>
A;Cross-references: GB:M77676; NID:G200058
A;Experimental source: A-LAK cells, C57BL
A;Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence
R;Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
J. Immunol. 149, 1957-1963, 1992
A;Title: Genomic structure and strain-specific expression of the natural killer cell
A;Reference number: A46502; MUID:92388663; PMID:1517565
A;Accession: A46502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109, 'H', '111-181', 'D', 183-227 <GI2>
A;Cross-references: GB:X64716; NID:G53395; PIDN:CAA45971.1; PID:G817989
A;Experimental source: BAUB/c 3T3 fibroblastoid cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072)
R;Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
J. Immunol. 147, 3229-3236, 1991
A;Title: cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of
A;Reference number: A46456; MUID:92013158; PMID:1680927
A;Accession: A46456
A;Molecule type: mRNA
A;Residues: 1-38, 'L', 40-227 <YOK>
A;Cross-references: GB:M77753; NID:G198569; PIDN:AAA39366.1; PID:G198570
A;Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 18.7%; Score 191; DB 2; Length 227;
Best Local Similarity 27.4%; Pred. No. 1.5e-10;
Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;

QY 24 PQQSSSSKPSCSCLVAITGLLT-PAVLLSVLLYQ-----WILCOGS-NYST-CASCPS 74
Db 34 PRSHRSALKLSCAGLILVVLIGMSVLRVLVLIQPSIEKCYVLQENLTKTDCSAKLE 93
QY 75 CPDRWMKYGNHCYFVSVEEKDWNSSLEFLCLARDSHLLVITDQMSLLQVFLSEAF--CW 132
Db 94 CPQDWLSHRDKCFHVSQVSNVTEEGLVDCDGKATMLIQDEELRFLDLSIKEKYNFV 153
QY 133 IGLR---NNSGWRWEDGSPNFS--RISSNFPVQTCGAINKNGLOASCEVPLHGVCCK 186
Db 154 IGLRYTLPMNWKWINGSTLNSDLVKITGDTENDSCAAISGDKVTFESCNSDNRWICOK 212

RESULT 5
PT0372
natural killer cell receptor group 2, splice form A - human
N;Alternate names: NKG2-A; NKG2-B
N;Contains: natural killer cell receptor group 2, splice form B
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
C;Accession: PT0372; PT0373
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I
A;Reference number: PT0372; MUID:91178434; PMID:2007850
A;Accession: PT0372
A;Molecule type: mRNA
A;Residues: 1-233 <HOU1>
A;Cross-references: EMBL:X54867; NID:G35056; PIDN:CAA38649.1; PID:G35057
A;Experimental source: natural killer cell
A;Accession: PT0373
A;Molecule type: mRNA
A;Residues: 1-95, 114-233 <HOU2>
A;Cross-references: GB:X54868; NID:G35058; PIDN:CAA38650.1; PID:G35059
A;Experimental source: natural killer cell
C;Genetics:
A;Gene: GDB:KLCR1; NKG2

A;Cross-references: GDB:138773; OMIM:161555
A;Map position: 12pter-12qter
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: alternative splicing; glycoprotein; transmembrane protein
F;71-98/Domain: transmembrane #status predicted <TRA>
F;119-229/Domain: C-type lectin homology <LCH>
F;102,103,151,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-130,147-229,208-221/Disulfide bonds: #status predicted

Query Match 18.6%; Score 190; DB 2; Length 233;
Best Local Similarity 27.8%; Pred. No. 1.9e-10;
Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;

QY 5 VIYSMLELPATQAQNDYGPQKSSSK--PSC-SCLVAITLGLTAVLL-----SVLLYQ 57
Db IT:IAELNLQASQ---DFQNDKTYHCKDLPSPAPEKLIVGLIGLILMASVVTVIIP 94
QY 58 WILQGSNYST-----CASPCSPDRWMKYGNHCYFVSVEEKDWNSSLEFCLARDSHL 110
Db STLIQRHNSNLNTRTKARHCHGCPREWITYNSCYIIGKERTWESLLACTSKNSSL 154
QY 111 LVITDQEMSLQVFLSEAFWIGL--RNSGWRWEDGSPINFNR--ISSNSFVQTCGAIN 167
Db LSIDNEEMKFLSIIPSS--WIGVFRNSHHPPWTWNGLAFAKHEIKDSNAELNCAVLQ 212
QY 168 KNGQLQASSCEVPLHGVC 185
Db 213 VNRLKSAQCSSIIYHCK 230

RESULT 6
PT0374
natural killer cell receptor group 2-C, splice form 1 - human
N;Alternate names: NKG2-C
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
C;Accession: PT0374
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II
A;Reference number: PT0372; MUID:91178434; PMID:2007850
A;Accession: PT0374
A;Molecule type: mRNA
A;Residues: 1-231 <HOU>
A;Cross-references: EMBL:X54869; NID:g35060; PIDN:CAA38651.1; PID:g35061
A;Experimental source: natural killer cell
C;Genetics:
A;Gene: GDB:KLRC2; NKG2-C
A;Cross-references: GDB:9787095
A;Map position: 12p13-12p13
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: glycoprotein; transmembrane protein
F;71-96/Domain: transmembrane #status predicted <TRA>
F;27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.8%; Score 182; DB 2; Length 231;
Best Local Similarity 27.8%; Pred. No. 1.1e-09;
Matches 47; Conservative 32; Mismatches 76; Indels 14; Gaps 5;

QY 24 PQKSSSSKPCSCCLVAITLGLTAVLLSVLLYQWILCOGSNYST-----CASPCSPDRW 79
Db PPEKLTAEVLGIICIV-----LMATVLKTVLTPFLFQNNSSPNTRTKARHCHGCPFEW 121
QY 80 MKYGNHCYFVSVEEKDWNSSLEFCLARDSHLIVITDQEMSLQVFLSEAFWIGL--RNN 138
Db IT:IAELNLQASQ---DFQNDKTYHCKDLPSPAPEKLIVGLIGLILMASVVTVIIP 94
QY 139 SGWRWEDGSPINFNR--ISSNSFVQTCGAINKNGLOASSCEVPLHGVC 185
Db 213 VNRLKSAQCSSIIYHCK 230

RESULT 7
PT0375
natural killer cell receptor group 2-D - human
N;Alternate names: integral membrane protein NKG2-D
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
C;Accession: PT0375; S15671; S19110
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I
A;Reference number: PT0372; MUID:91178434; PMID:2007850
A;Accession: PT0375
A;Molecule type: mRNA
A;Residues: 1-216 <HOU>
A;Cross-references: EMBL:X54870; NID:g35062; PIDN:CAA38652.1; PID:g35063
A;Experimental source: natural killer cell
A;Note: translation of nucleotide sequence is not complete
C;Keywords: transmembrane protein

Query Match 17.6%; Score 180; DB 2; Length 216;
Best Local Similarity 26.8%; Pred. No. 1.6e-09;
Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY 37 CLVAITLGL-----LLTAVLLSVLLYQWILCOGSNYSTCASPCSPDRWKMKYGNHCY 88
Db CFTAVANGIRPITMVAISAVFLNSLENQEVQIP-----LTESYCGPCPKWICYKNKCYQ 112
QY 89 FSVEEKDWNSSLEFCLARDSHLIVITDQEMSLQVFLSEAFWIGL--RNSGWRWED 145
Db FFDESKNWSYEQASCMSQNASLILKYSKEDQDLK--LVKSYHWMGLVHIPTNGSQWQWED 170
QY 146 GSPINFRI-----SSNSFVQTCGAIN 167
Db 171 GSTLSPNLLTIEMQKDCALYASSPKGYIENCSTEN 207

RESULT 8
I54524
natural killer cell receptor group 2-C, splice form 2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 19-May-2000
C;Accession: I54524
R;Adamkiewicz, T.V.; McSherry, C.; Bach, F.H.; Houchins, J.P.
Immunogenetics 39, 218, 1994
A;Title: Natural killer lectin-like receptors have divergent carboxy-termini, distinct
A;Reference number: I54524; MUID:94102823; PMID:8276468
A;Accession: I54524
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-240 <RES>
A;Cross-references: GB:L14542; NID:g292360; PIDN:AAAI6833.1; PID:g292361
C;Genetics:
A;Gene: GDB:KLRC2; NKG2-C
A;Cross-references: GDB:9787095
A;Map position: 12p13-12p13
C;Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match 17.4%; Score 178.5; DB 2; Length 240;
Best Local Similarity 28.6%; Pred. No. 2.4e-09;
Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 24 PQKSSSSKPCSCCLVAITLGLTAVLLSVLLYQWILCOGSNYST-----CASPCSPDRW 79
Db PPEKLTAEVLGIICIV-----LMATVLKTVLTPFLFQNNSSPNTRTKARHCHGCPFEW 121
QY 80 MKYGNHCYFVSVEEKDWNSSLEFCLARDSHLIVITDQEMSLQVFLSEAFWIGL--RNN 137
Db IT:IAELNLQASQ---DFQNDKTYHCKDLPSPAPEKLIVGLIGLILMASVVTVIIP 94
QY 122 ITYSNSCYIIGKERTWESLLACTSKNSSLIDNEEIKFLASILPSS--WIGVFRNS 179
QY 138 NSGWRWEDGSPINFNR--ISSNSFVQTCGAINKNGLOASSCEVPLHGVC 176
Db 180 SHHPWVTINGLAFAKHEIKDSNAELNCAVLQVRLKSAQCSSIIYHCK 228

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:41 ; Search time 7.35929 Seconds
(without alignments)
1337.256 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLELPATQAN.....GLQASSCEVPLHGVCVKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	199	19.5	233	1	1	1	Q95mi5 pan troglod
2	198.5	19.4	179	1	1	1	Q9mkz9 macaca mula
3	196.5	19.2	179	1	1	1	Q13241 homo sapien
4	196.5	19.2	199	1	1	1	CD69 MOUSE
5	194.5	19.0	179	1	1	1	CD94 PANTR
6	191	18.7	227	1	1	1	NK11 MOUSE
7	190	18.6	233	1	1	1	NKGA HUMAN
8	187	18.3	233	1	1	1	NKGC PANTR
9	186	18.2	231	1	1	1	NKGD HUMAN
10	183.5	17.9	216	1	1	1	NKGD MACMU
11	183	17.9	233	1	1	1	NKGD MACMU
12	180	17.6	216	1	1	1	NKGD HUMAN
13	178.5	17.4	240	1	1	1	NKGE HUMAN
14	177.5	17.4	240	1	1	1	NKGE PANTR
15	175.5	17.2	223	1	1	1	NK13 RAT
16	175	17.1	149	1	1	1	CLE2 HUMAN
17	174.5	17.1	304	1	1	1	MMGL MOUSE
18	174	17.0	199	1	1	1	CD69 HUMAN
19	167	16.3	301	1	1	1	LECI MOUSE
20	164.5	16.1	306	1	1	1	MMGL RAT
21	163.5	16.0	283	1	1	1	LECH MOUSE
22	163	15.9	231	1	1	1	NKGC MACMU
23	162	15.8	262	1	1	1	LY4A MOUSE
24	160.5	15.7	223	1	1	1	NK12 MOUSE
25	160.5	15.7	283	1	1	1	LECH RAT
26	157.5	15.4	290	1	1	1	LECH HUMAN
27	156.5	15.3	163	1	1	1	V239 FOWPV
28	156.5	15.3	301	1	1	1	LECI RAT
29	153.5	15.0	167	1	1	1	V008 FOWPV
30	151.5	14.8	263	1	1	1	NK14 MOUSE
31	148.5	14.5	220	1	1	1	KLR4 MOUSE
32	148.5	14.5	550	1	1	1	KUCR RAT
33	147.5	14.4	175	1	1	1	PBCG_MESAU

34	147	14.4	174	1	1	1	PAP3 MOUSE
35	146.5	14.3	548	1	1	1	KUCR MOUSE
36	146	14.3	117	1	1	1	CHBB CROHO
37	146	14.3	311	1	1	1	LECI HUMAN
38	141.5	13.8	1458	1	1	1	PA2R_RABIT
39	140.5	13.7	280	1	1	1	KLR7 MOUSE
40	139.5	13.6	3562	1	1	1	PGCV_CHICK
41	138.5	13.5	1463	1	1	1	PA2R_BOVIN
42	137.5	13.4	175	1	1	1	PAP1 MOUSE
43	137	13.4	165	1	1	1	LITH RAT
44	136.5	13.3	321	1	1	1	FCE2_HUMAN
45	136.5	13.3	331	1	1	1	FCE2_MOUSE

ALIGNMENTS

RESULT 1

ID	NKGA_PANTR	STANDARD;	PRT;	233 AA.
AC	Q95MI5; Q9MYM6;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating NK receptor) (NK cell receptor A).			
DE	NK receptor (NK cell receptor A).			
GN	KLRCl OR NKG2A.			
OS	Pan troglodytes (Chimpanzee).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.			
OX	NCBI_TaxID=9598;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=20350666; PubMed=10894168;			
RA	Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L., Muir D.G., Canavez F., Cooper S.I., Valiante N.M., Lanier L.L., Parham P.;			
RA	Parham P.;			
RT	"Rapid evolution of NK cell receptor systems demonstrated by comparison of chimpanzees and humans."			
RL	Immunity 12:687-698(2000).			
[2]				
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS LEU-79 AND ARG-231.			
RP	MEDLINE=21623899; PubMed=11751968;			
RA	Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P.;			
RA	"Conservation and variation in human and common chimpanzee CD94 and NKG2 genes."			
RL	J. Immunol. 168:240-252(2002).			
CC	-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.			
CC	-!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=NKG2-A;			
CC	Isoid=Q95MI5-1; Sequence=Displayed;			
CC	Name=NKG2-B;			
CC	Isoid=Q95MI5-2; Sequence=VSP_003066;			
CC	-!- TISSUE SPECIFICITY: Natural killer cells.			
CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.			

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EMBL; AF259055; AAF86965.1; -;
EMBL; AF259056; AAF86966.1; -;
EMBL; AF350005; AAK83792.1; -;


```

Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;
QY 17 QAQNDYGFQ---QKSSSKPSCSCVATITLGLTAVLLSVLLYQWILCOGNSYSTCASCSP 73
Db 18 RGQKDHGTSIHFEKHGEG---SIQVSIPIWAVLIVLITSLIIALIANVCKY-----NCP 69
QY 74 -----SCPRMWMKGNHCYFVSVEEKDNSSLEFCIARDSHLLVITDQEM 119
Db 70 GLYEKLSSDHHVATCKNEWTSYRTCYFFFTTKSWALAQSCSDAATLAVIDSEKDM 129
QY 120 SLLQVFLSEAPFCWTGLRN--NSGWRWEDGSPIN--FSRISNSFVOTCGAINKNGLOASS 175
Db 130 TFLKRYSGELEHWIGLKEANQTKWANGKEFNWFLTGSG-----RCVSNHKNVTAVD 185
QY 176 CEVPLHGVCKK 186
Db 186 CEANFHWVCSK 196

RESULT 5
CD94_PANTR
ID CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9MZ41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20350666; PubMed=10894168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
RA Parham P.;
RT "Rapid evolution of NK cell receptor systems demonstrated by
RT comparison of chimpanzees and humans.";
RL Immunity 12:687-698(2000).
[2]
RN ALTERNATIVE SPLICING.
RX MEDLINE=21623989; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms seem to exist;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MZ41-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MZ41-2; Sequence=VSP_003056;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
-----
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DR EMBL; AF259054; AAF86964.1; -.
DR HSP; P22897; 1EGG.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SMO0034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10
FT TRANSMEM 11 31
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 32 179
FT DOMAIN 98 176
FT DISULFID 61 72
FT DISULFID 89 174
FT DISULFID 152 166
FT CARBOHYD 83 83
FT CARBOHYD 132 132
FT VARSPLIC 105 105
FT /FTid=VSP_003056.
SQ SEQUENCE 179 AA; 20493 MW; 7244D99ED9587E7 CRC64;

Query Match 19.0%; Score 194.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 1.3e-11;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCVAITGLTAVLLSVLLVQLCOGSN--YSTCASCPCDPDMWKNHCYFVSVE 92
Db 20 CLSLMA-TLGLLKNSFTKLSEIAPFTGPNIELQKDSQCQCKWGVRCNCFYSSE 78
QY 93 EKDWNSSLEFCLARDSHLLVITDQEMSLLOVFLSEAFVCLGL--RNNSCWRWEDGSP 149
Db 79 QKTWNRSHLCASQKSSLLQLQNTDELDFMS--SSQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFRSISNSF---VQTGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLPFSFTFNPKNCIAVNPNGNALDESCDKNRYICKQ 176

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RESULT 6

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NK11_MOUSE
ID NK11_MOUSE STANDARD; PRT; 227 AA.
AC P27811;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein P1-2 (NKR-P1 2) (NKR-P1.7).
GN KLRB1A OR LY55A OR LY55.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giordano R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells."
RL J. Immunol. 147:1701-1708 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013159; PubMed=1680927;
RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
RA Seaman W.E.;
RT "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
RT Identification of a natural killer cell gene complex on mouse
RT chromosome 6."
RL J. Immunol. 147:3229-3236 (1991).
CC -I- FUNCTION: May function as signal-transmitting receptor.
CC -I- SUBUNIT: Homodimer; disulfide-linked.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
CC -I- TISSUE SPECIFICITY: Natural killer cells.

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CC

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CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; M77676; AAA39822.1; -.
DR EMBL; M77253; AAA39366.1; -.
DR PIR; A46467; A46467.
DR HSP; P22897; 1EGG.
DR MGD; MGI:107540; Klrbl1a.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SMO0034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 42
FT TRANSMEM 43 62
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 63 227
FT DOMAIN 93 212
FT DISULFID 94 105
FT DISULFID 122 210
FT DISULFID 189 202
FT CARBOHYD 83 83
FT CARBOHYD 169 169
FT CARBOHYD 186 186
FT CONFLICT 39 39
SQ SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;

Query Match 18.7%; Score 191; DB 1; Length 227;
Best Local Similarity 27.4%; Pred. No. 3.8e-11;
Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7;

QY 24 PQQSSSSKSCSLVAITGLL-TAVLLSVLLVQ-----WILCOGS-NYST-CASCPS 74
Db 34 PRSHRSALKSLSCAGLLVLLVTLGMSVLVRLVLPKPSIEKCYVLIQENLAKNTDCSAKLE 93
QY 75 CPDRWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLLOVFLSEAF--CW 132
Db 94 CPQDWLSHRDKCFHVSQVSNVWEEGLVDCGKGATLMLIQDEELRFLLSIKEKNSFW 153
QY 133 IGLR---NNSGWRWEDGSPINFS--RISNSFVQTGAINKNG-LQASSCEVPLHGVCCK 186
Db 154 IGLRYTLPMNWKWINGSTLNSDLVKITGTENDSCAAISGDKVTFESCSNDRNWCQK 212

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RESULT 7

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NKGA_HUMAN
ID NKGA_HUMAN STANDARD; PRT; 233 AA.
AC P26715;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NK2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
DE NK receptor) (NK cell receptor A).
GN KLRC1 OR NKG2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones

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RT encoding type II integral membrane proteins on human natural killer
RT cells."; Med. 173:1017-1020(1991).
RL [2]
RN J. Exp. Med. 173:1017-1020(1991).
RP SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
RX MEDLINE=96337918; PubMed=8753859;
RA Plougastel B., Jones T., Trowsdale J.;
RT "Genomic structure, chromosome location, and alternative splicing of
RT the human NKG2A gene.";
RL Immunogenetics 44:286-291(1996).
[3]
RN SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
RX MEDLINE=98260668; PubMed=9598306;
RA Plougastel B., Trowsdale J.;
RT "Sequence analysis of a 62-kb region overlapping the human KLR2
RT cluster of genes.";
RL Genomics 49:193-199(1998).
[4]
RN SEQUENCE FROM N.A.
RA Kothapalli R., Kusmartseva I., Loughran T.P. Jr.;
RT "Identification and characterization of the NKG2A gene from large
RT granular lymphocytic leukemia (LGL) cells.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.U., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NKG2-A;
CC IsoId=P26715-1; Sequence=Displayed;
CC Name=NKG2-B;
CC IsoId=P26715-2; Sequence=VSP_003062;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC -----
CC EMBL; X54867; CAA38649.1; -
CC EMBL; X54868; CAA38650.1; -
CC EMBL; U54786; AAB17133.1; -
CC EMBL; U54783; AAB17133.1; JOINED.
CC EMBL; U54784; AAB17133.1; JOINED.

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DR EMBL; U54785; AAB17133.1; JOINED.
DR EMBL; AF023840; AAC17488.1; -
DR EMBL; AF461812; AAL65234.1; -
DR EMBL; BC012550; AAHL2550.1; -
DR EMBL; BC053840; AAH53840.1; -
DR PIR; PT0372; PT0372.
DR Genew; HGNC:6374; KLRCL.
DR MIM; 161555; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; LECTIN_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00441; C_TYPE_LLECTIN_2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Alternative splicing.
KW DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
KW TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
KW DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).
KW DOMAIN 118 231 C-TYPE LECTIN (LONG FORM).
KW DISULFID 119 130 BY SIMILARITY.
KW DISULFID 147 229 BY SIMILARITY.
KW DISULFID 208 221 BY SIMILARITY.
KW CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW VARSPLIC 96 113 Missing (in isoform NKG2-B).
/FTid=VSP_003062.
SQ SEQUENCE 233 AA; 26287 MW; 1654BD7958C81A84 CRC64;
Query Match 18.6%; Score 190; DB 1; Length 233;
Best Local Similarity 27.8%; Pred. No. 4.9e-11;
Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;
QY 5 VIYSMLELPTAQNDYGPQKSSSK--PSC-SCLVAITGLLTAVLL---SVLLYQ 57
Db 38 ITYAEINLQKASQ----DFQNDKTYHCKDLFAPEKLIVGLIGILIMASVTVIIP 94
QY 58 WILCOGSNYST-----CASCPCDPRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHL 110
Db 95 STLIQRHNSSSLNTRTQXARHCHGCPPEWITYNSCYIYIGKRRRTWEESLLACTSKNSSL 154
QY 111 LVITDQNMQLLOVFLSEAFWIGL--RNNSGWRWEDGSPINFSR--ISSNSFVQCGAIN 167
Db 155 LSIDNEEMKFLSIIPSS--WIGVFRNSSHPWVTMNGLAFKHEIKDSNDELCAVLQ 212
QY 168 KNGLOASSCEVPLHGVC 185
Db 213 VNRLSAQCGSSIIYHCK 230
RESULT 8
NKG2C_PANTR
ID NKG2C_PANTR STANDARD; PRT; 233 AA.
AC Q9GME8; Q9MZ38; Q9MZ40;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE NKG2-C type II integral membrane protein (NKG2-C activating NK
DE receptor) (NK cell receptor C).
DE KLR2 OR NKG2C.
GN Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-60 AND 232-TYR-ARG-233 DEL.
RX MEDLINE=20350666; PubMed=10894168;

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FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 2 2 S -> N (in allele NKG2-C*02).
FT VARIANT 102 102 /FTid=VAR_013404.
FT VARIANT 161 161 S -> F (in allele NKG2-C*02).
FT CONFLICT 161 161 /FTid=VAR_013405.
FT SEQUENCE 231 AA; 26072 MW; 6B971EECD7542930 CRC64;
Query Match 18.2%; Score 186; DB 1; Length 231;
Best Local Similarity 28.4%; Pred. No. 1.2e-10;
Matches 48; Conservative 31; Mismatches 76; Indels 14; Gaps 5;
QY 24 PQKSSSSKPCSCCLVAITLGLTAVLLSVLLQYLQWILCOGQSNYSF---CASCPCSPDRW 79
DB 67 PPEKLTAEVLGIICIV-----LMAIVLKIIVLIPLEQNNSSPNRTQKARHCHGCPPEW 121
QY 80 MKNYGNHCYFVSVEEKDNSSLEFCLARDSHLIVITDQEMSLQLQVFLSEAFQWIGL-RNN 138
DB 122 IYNSCYIYIGKERTWESLLACTSKNSLLSIDNEEMKFLASILPSS--WIGVERNS 179
QY 139 SGWRWEDGSPINFSR--ISSNSFVOTCGAINKNGLOASCEVPLHGVCV 185
DB 180 SHHPWVTINGLAFKHKIDSDNAELNCALVQVNRKLSAQCGSSMIYHCK 228

RESULT 10
NKGD MACMU
ID NKGD MACMU STANDARD; PRT; 216 AA.
AC Q9MZJ7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor) (NK cell receptor D).
GN NKGD.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; AF190943; AAF74539.1; -.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT. 1.
CC PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism.
FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 73 216 (POTENTIAL).
FT DOMAIN 98 213 EXTRACELLULAR (POTENTIAL).
FT DISULFID 99 110 C-TYPE LECTIN (LONG FORM).
FT DISULFID 127 211 BY SIMILARITY.
FT CARBOHYD 189 203 BY SIMILARITY.
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 216 AA; 25075 MW; A44893F31400DEAC CRC64;
Query Match 17.9%; Score 183.5; DB 1; Length 216;
Best Local Similarity 26.2%; Pred. No. 1.9e-10;
Matches 49; Conservative 40; Mismatches 75; Indels 23; Gaps 6;
QY 15 ATQANDYGPQOKS-----SSKPCSCCLVAITLG-----LLTAVLLSVLLQWILCO 62
DB 31 STRCQKQPCVIKSKRENASPLFFCCFIAMGIRFIMVTINSAVFLNSLFNQEVQIP 90
QY 63 GSNYSTCASCPCSPDRWMKYNHCYFVSVEEKDNSSLEFCLARDSHLIVITDQEMSL 122
DB 91 -----LTESYCGPCPNWICYKNVCYQFFNESKNWYESQASCSQNASLLKYSKEDQDL 146
QY 123 QVFLSEAFQWIGL---RNSGWRWEDGSPINFSNSFVOTCGAINKNGLOA--SSCE 177
DB 147 K-LVKSVHYVHGLVHIPNGSWQEDGSLPNLLITTEMQKDCALYASSFKGYIENS 204
QY 178 VPLHGVC 184
DB 205 IPTYVIC 211

RESULT 11
NKGA MACMU
ID NKGA MACMU STANDARD; PRT; 233 AA.
AC Q9MZJ3; Q9MZI8; Q9MZJ0; Q9MZJ1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating
DE NK receptor) (NK cell receptor A).
GN NKGA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS NKG2-A; NKG2-ADTM; NKG2-B AND NKG2-BDTM).
RX MEDLINE=20322487; PubMed=10866118;
RA LaBonte M.L., Levy D.B., Letvin N.L.;
RT "Characterization of rhesus monkey CD94/NKG2 family members and
RT identification of novel transmembrane-deleted forms of NKG2-A, B, C,
RT and D.";
RL Immunogenetics 51:496-499(2000).
CC -!- FUNCTION: plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=NKG2-A;
CC IsoId=Q9MZJ3-1; Sequence=Displayed;
CC Name=NKG2-B;
CC IsoId=Q9MZJ3-2; Sequence=VSP_003064;
CC Name=NKG2-Adtm;
CC IsoId=Q9MZJ3-3; Sequence=VSP_003063;
CC Name=NKG2-Bdtm;
CC IsoId=Q9MZJ3-4; Sequence=VSP_003065;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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-----
EMBL; AF190979; AAF73835.1; -
EMBL; AF190981; AAF73837.1; -
EMBL; AF190982; AAF73838.1; -
EMBL; AF190984; AAF73840.1; -
HSP; P22897; IEGG.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLCCT; 1.
PROSITE; PS00615; C TYPE LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C TYPE LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
Glycoprotein; Alternative splicing.
FT DOMAIN 1 70
FT TRANSMEM 71 93
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 94 233
FT EXTRACELLULAR (POTENTIAL).
FT C-TYPE LECTIN (LONG FORM).
FT BY SIMILARITY.
FT DISULFID 119 130
FT DISULFID 147 229
FT DISULFID 208 221
FT CARBOHYD 102 102
FT CARBOHYD 103 103
FT CARBOHYD 151 151
FT VARSPPLIC 63 95
FT (in isoform NKG2-Adtm).
FT FTID=VSP 003063.
FT VARSPPLIC 96 113
FT Missing (in isoform NKG2-B).
FT FTID=VSP 003064.
FT VARSPPLIC 63 112
FT Missing (in isoform NKG2-Bdtm).
FT FTID=VSP 003065.
SQ SEQUENCE 233 AA; 26286 MW; 237B2BE3E489E76 CRC64;
Query Match 17.9%; Score 183; DB 1; Length 233;
Best Local Similarity 27.5%; Pred. No. 2.3e-10;
Matches 52; Conservative 34; Mismatches 81; Indels 22; Gaps 7;
QY 5 VIYSMLLPATQANDYGPQKSSSKPSCSC---LVAITLGLLTAVLL---SVLLYQ 57
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
38 ITVAELMLQKTSQ---DFQGNKNTNCKDLISAPEKLIAGILGICLVLMASVVTIVIP 94
QY 58 WILCOGSNYST-----CASCPCDPKWKYGNHCYVSVVEKDNSSLEFCLARDSHL 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95 STITQKHNNSSLNTRTQKARHCGHCPEWITYNSCYIIGKRRKTWAESLLACTSKNSSL 154
QY 111 LVITDQEMSLLOVFLSEAFWIGL-RNNSGWRWEDGSPNFSR--TSSNSFVQTGAIN 167
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
155 LSLDNEEMFLTAITLSS--WIDVFDSSHHPVWTINGLTFRKHEIKESDHAENCAMLH 212
QY 168 KNGIQASSC 176
Db : : : : :
213 VRGLFSDEC 221
RESULT 12
NKG2D HUMAN
ID NKG2D HUMAN STANDARD; PRT; 216 AA.
AC P26718; Q9NR41;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
GN receptor) (NK cell receptor D).
OS Homo sapiens (Human).

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```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach P.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehrach H., Hofer E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the
RT human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Kothapalli R., Kusmartseva I., Loughran T.P. Jr.;
RT "Identification and characterization of the NKG2D gene from large
RT granular lymphocytic leukemia (IGL) cells.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT THR-72.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guthlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -I- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
CC -I- TISSUE SPECIFICITY: Natural killer cells.
CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
EMBL; X54870; CAA38652.1; -.

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DR EMBL; AJ001687; CAA04925.1; -.
DR EMBL; AJ001688; CAA04925.1; JOINED.
DR EMBL; AJ001689; CAA04925.1; JOINED.
DR EMBL; AF461811; AAL65233.1; -.
DR EMBL; AF260135; AAF86973.1; -.
DR EMBL; AF260136; AAF86974.1; -.
DR EMBL; BC039836; AAK39836.1; -.
DR PIR; PT0375; PT0375.
DR PDB; 1HYR; 23-MAY-01.
DR PDB; 1KCG; 09-JAN-02.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. .; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism; 3D-structure.
FT DOMAIN 1 51
FT TRANSMEM 52 72
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 73 216
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 213
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 99 110
FT BY SIMILARITY.
FT DISULFID 127 211
FT BY SIMILARITY.
FT CARBOHYD 131 131
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 72 72
FT A -> T (in allele NKG2-D*02).
/FTID=VAR 013295.
SQ SEQUENCE 216 AA; 25274 MW; C22F6BD533D7800E CRC64;
Query Match 17.6%; Score 180; DB 1; Length 216;
Best Local Similarity 26.8%; Pred. No. 4e-10; 52; Indels 32; Gaps 5;
Matches 42; Conservative 31; Mismatches 11;
QY 37 CLVAITLG-----LITAVLLSVLLQWILCOGSNSTSCASCPCDRMKYGNHCY 88
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57 CFIAVAMGIRFLIMVAWSAVFLSNFQEVQIP---LTSYCGPCPKWICYKNVCYQ 112
QY 89 PSVEKDNSSLEFCLARDSHLVITDQMSLLQVFLSEAPCWGL---RNNSCWRWD 145
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
113 PFDESKNYESQASCMQSNASLLKYSKEDQDLK--LVKSYHWMGLVHIPITNGSQWED 170
QY 146 GSPINFSRI-----SSNSGFVOTCGAIN 167
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
171 GSILSPNLTITMOKGDCALYASSFKGYIENCSTPN 207

RESULT 13
ID NKGE HUMAN STANDARD; PRT; 240 AA.
AC Q07444; Q96RL0; Q9UP04;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2002 (Rel. 41, Last annotation update)
DE NKG2-E type II integral membrane protein (NKG2-E activating NK
DE receptor) (NK cell receptor E).
GN KLRG3 OR NKG2E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM NKG2-E).
RX MEDLINE=94102823; PubMed=8276468;
RA Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;
"Natural killer lectin-like receptors have divergent carboxy-termini,
distinct from C-type lectins.";
Immunogenetics 39:218-218(1994).
[2]
RP SEQUENCE FROM N.A. (ISOFORM NKG2-E).
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
Lehrach H., Hofer E., Francis P.;
"The genomic organization of NKG2C, E, F, and D receptor genes in the
human natural killer gene complex.";
Immunogenetics 48:163-173(1998).
[3]
RP SEQUENCE FROM N.A. (ISOFORM NKG2-H).
RX MEDLINE=99218418; PubMed=10201920;
RA Bellon T., Heredia A.B., Llano M., Minguella A., Rodriguez A.,
Lopez-Botet M., Aparicio P.;
"Triggering of effector functions on a CD8+ T cell clone upon the
aggregation of an activatory CD94/kp39 heterodimer.";
J. Immunol. 162:3996-4002(1999).
[4]
RP SEQUENCE FROM N.A. (ISOFORM NKG2-E), AND VARIANT ARG-19.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
"Conservation and variation in human and common chimpanzee CD94 and
NKG2 genes.";
J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=NKG2-E;
IsoId=Q07444-1; Sequence=Displayed;
Name=NKG2-H;
IsoId=Q07444-2; Sequence=VSP 003067;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC -----
CC EMBL; L14542; AAA16833.1; -.
CC EMBL; AJ001685; CAA04923.1; -.
CC EMBL; AF078550; AAD46108.1; -.
CC EMBL; AF350016; AAK83803.1; -.
CC EMBL; AF350017; AAK83804.1; -.
CC PIR; I54524; I54524.
CC HSP; P05451; ILIT.
CC HSP; HGNC:6376; KLRG3.
CC MIM; 602892; -.
CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC InterPro; IPR001304; Lectin C.
CC Pfam; PF00059; lectin C; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
CC PROSITE; PS00411; C-TYPE LECTIN 2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Alternative splicing; Polymorphism.
FT DOMAIN 1 70
FT TRANSMEM 71 93
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 94 240
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 230
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128
FT BY SIMILARITY.
FT DISULFID 207 220
FT BY SIMILARITY.

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FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 227 240 RRGIMLTRVLVNS -> VSISFRIKALELAVHQIKFYICS
FT NRNDIMIA (in isoform NKG2-H).
FT /FTid=VSP 003067.
FT VARIANT 19 19 P -> R (in allele NKG2-B*02).
FT /FTid=VAR 013296.
FT VARIANT 135 135 R -> S (in dbSNP:1138437).
FT /FTid=VAR 014560.
SQ SEQUENCE 240 AA; 27012 MW; 20691F82174D8A6 CRC64;

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Query Match 17.4%; Score 178.5; DB 1; Length 240;
 Best Local Similarity 28.6%; Pred. No. 6.3e-10;
 Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

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QY 24 PQQSSSKPSCSCLVAITLGLTAVLLSVLLYQWILCOGSNYST----CASCPCSPDRW 79
DB 67 PPEKLTAVLGIICIV-----LMAVLKTIVLIPFLEQNNSSPNTRTQKARPCGHCPEEW 121
QY 80 MKYGNHCYFVSVEKDNWSLFLCLARDSHLLVITDN-QEMSLQVLFSEAFWIGL-RN 137
DB 122 ITYSNSCYITGKERTWEESLQACASKNSSLLSIDNEEMKFLASILPSS--WIGVFN 179
QY 138 NSGRWEDGSPFNFSR--IGSNSFVQTCGAINKNGLOASSC 176
DB 180 SSHPWVTINGLAFKHEIKDSHAERNCAHLVHVGSLISDQC 220

```

RESULT 14

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NKGE PANTR STANDARD; PRT; 240 AA.
AC Q95MT4; Q95MT3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKG2-E type II integral membrane protein (NKG2-E activating NK
DE receptor) (NK cell receptor E).
GN KLRC3 OR NKG2E.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT ARG-213.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF350006; AAK83793.1; -
DR EMBL; AF350007; AAK83794.1; -
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

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```

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein; Polymorphism.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 94 240 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 230 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 207 220 BY SIMILARITY.
FT VARIANT 213 213 C -> R (IN NKG2-E*02).
SQ SEQUENCE 240 AA; 26996 MW; BC28FB3CEA93A5E0 CRC64;

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Query Match 17.4%; Score 177.5; DB 1; Length 240;
 Best Local Similarity 28.0%; Pred. No. 7.9e-10;
 Matches 45; Conservative 30; Mismatches 71; Indels 15; Gaps 5;

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QY 24 PQQSSSKPSCSCLVAITLGLTAVLLSVLLYQWILCOGSNYST----CASCPCSPDRW 79
DB 67 PPEKLTAKMGIICIV-----LMSAVLKTIVLIPFLEQNNSSPNTRTQKARPCGHCPEEW 121
QY 80 MKYGNHCYFVSVEKDNWSLFLCLARDSHLLVITDN-QEMSLQVLFSEAFWIGLRNN 138
DB 122 ITYSNSCYITGKERTWEESLQACASKNSSLLSIDNEEMKFLASILPSS--WIGVFN 179
QY 139 SG---RWEDGSPFNFSRISNSFVQTCGAINKNGLOASSC 176
DB 180 SSHPWVTINGLAFKHEIKDSHAERNCAHLVHVGSLISDQC 220

```

RESULT 15

```

NK13 RAT STANDARD; PRT; 223 AA.
AC P27471;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen
DE 3.2.3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90378305; PubMed=2399464;
RA Giorda R., Rudert W.A., Vavassori C., Chambers W.H.,
RA Hiserodt J.C., Trucco M.;
RT "NKR-P1, a signal transduction molecule on natural killer cells.";
RL Science 249:1298-1300(1990).
CC -!- FUNCTION: Mediates transmembrane signaling in natural killer
CC (NK) cells and so may act as a receptor able to selectively
CC trigger NK cell activity.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- MISCELLANEOUS: Ligand binding may be calcium dependent.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; M62891; AAA41710.1; -
DR PIR; A35917; A35917.
DR HSP; P22897; 1EGG.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.

```

```
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 94 105 BY SIMILARITY.
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

Query Match 17.2%; Score 175.5; DB 1; Length 223;
Best Local Similarity 27.1%; Pred. No. 1.1e-09;
Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 PQOKSSSKPSCSLVAITLGLL-TAVLLSVLLYQ-----WILQGSNYSTCASCPS-- 74
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35 PRSHRLALKSCAGLILVLALVGMSSILVRVLVQPSVEPCRVLIQ-ENLSKTGS-PAKL 92
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 -CPDRWMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLLOVF---LSEAF 130
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 KCPKDWLSHRDKCFHVQSITWKESLADCGKGATLLLVQDQELRFLRNLTKEISSSF 152
QY 131 CWIGLR---NNSGWEDGSPINFS--RISNSFVQTCGAINKNGLQASSCEVPLHGVC 185
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 -WIGLSYTLSDENWKWINGSTLNSDVLSTGTEDKSCASVSQDKVLSQCDSDNIWVCQ 211
QY 186 K 186
DB 212 K 212
```

Search completed: August 10, 2004, 16:16:59
Job time : 8.35929 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:01 ; Search time 46.8319 Seconds
(without alignments)
1140.281 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDVIVSMLELPATQAN.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1023	100.0	189	2	AAW88265
2	1023	100.0	189	4	AAE11759
3	1007	98.4	189	7	ADD25635
4	789	77.1	843	4	ABG05451
5	548.5	53.6	188	4	AAE11760
6	525.5	51.4	188	2	AAE117033
7	525.5	51.4	188	2	AAW88277
8	525.5	51.4	188	4	AAE11761
9	431	42.1	99	2	AAW88267
10	370.5	36.2	114	2	AAE117472
11	306.5	30.0	70	2	AAW88266
12	230	22.5	231	5	ABB1897
13	226	22.1	198	4	AAW88815
14	226	22.1	198	4	AAU19820
15	226	22.1	198	5	ABP48040
16	226	22.1	198	7	ADC11002
17	226	22.1	203	4	AAU19659
18	226	22.1	203	5	ABP47879
19	226	22.1	203	7	ADC10841
20	217	21.2	35	4	AAU14192
21	217	21.2	35	4	ABB33139
22	217	21.2	35	4	AAW26602
23	217	21.2	35	4	ABB27967
24	217	21.2	35	4	ABB18604
25	217	21.2	35	4	AAW66323

26	217	21.2	35	4	AAW53935	Human bra
27	217	21.2	35	4	ABG47989	Human liv
28	217	21.2	35	4	AAW01928	Peptide #
29	217	21.2	35	5	ABG35971	Human pep
30	216.5	21.2	182	4	AAU19660	Human nov
31	216.5	21.2	182	5	ABP47880	Human pol
32	216.5	21.2	182	7	ADC10842	Human ext
33	201	19.6	225	2	AAW65189	NK cell a
34	197	19.3	218	4	AAW65189	Murine mO
35	196.5	19.2	179	2	AAW64791	Human Kp4
36	196.5	19.2	179	2	AAW40222	CD94. 7/1
37	196.5	19.2	179	8	ADE76965	Human pro
38	196.5	19.2	199	2	AAW54660	Murine CD
39	196.5	19.2	199	2	AAW55595	Mouse CD6
40	195.5	19.1	278	4	AAW5871	O. cunicu
41	194	19.0	268	6	ABJ19328	NOVX rela
42	194	19.0	276	6	AAE37769	Human C-t
43	193	18.9	257	2	AAW85594	Chicken 1
44	193	18.9	270	2	AAW95586	Low dens1
45	193	18.9	270	2	AAW24152	Bovine ID

ALIGNMENTS

RESULT 1
AAW88265

ID AAW88265 standard; protein; 189 AA.

XX AC AAW88265;

XX 29-MAR-1999 (first entry)

XX Human mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; splice variant; human;
inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 7..10

XX Modified-site /note= "ITIM motif"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

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XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX Modified-site /note= "Asn is N-glycosylated"

XX This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAW84198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC KUB12 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AAW88277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
 CC an extracellular lectin-like domain. 2 Alternately spliced forms (see
 CC AAW88266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AAW88258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDSVIYMLELPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 DB 1 MTDSVIYMLELPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 CQGSNYSTCASCPCPDRAWKMYGNHCYFVSVEEKDWNSSLBFLCLARDSHLLVITDQEMS 120
 DB 61 CQGSNYSTCASCPCPDRAWKMYGNHCYFVSVEEKDWNSSLBFLCLARDSHLLVITDQEMS 120
 QY 121 LLOVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVQTCGAINKNGLOASCEVPL 180
 DB 121 LLOVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVQTCGAINKNGLOASCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 2

AAE11759
 ID AAE11759 standard; protein; 189 AA.

XX AAE11759;
 AC AAE11759;
 DT 18-DEC-2001 (first entry)
 XX Human mast cell function associated antigen (MAFA) protein.
 DE Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX Homo sapiens.
 OS WO200170805-A2.
 XX 27-SEP-2001.
 XX 16-MAR-2001; 2001WO-US008596.
 XX 17-MAR-2000; 2000US-0190716P.
 XX (GEMI-) GEMINI SCI INC.
 XX Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 DR N-PSDB; AAD18734.
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX Claim 10; Page 18; 49pp; English.

CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 XX

SQ Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDSVIYMLELPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 DB 1 MTDSVIYMLELPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 CQGSNYSTCASCPCPDRAWKMYGNHCYFVSVEEKDWNSSLBFLCLARDSHLLVITDQEMS 120
 DB 61 CQGSNYSTCASCPCPDRAWKMYGNHCYFVSVEEKDWNSSLBFLCLARDSHLLVITDQEMS 120
 QY 121 LLOVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVQTCGAINKNGLOASCEVPL 180
 DB 121 LLOVFLSAFCWIGLRNNSGWRWEDGSPINFSTRSSNSFVQTCGAINKNGLOASCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 3

ADD25635
 ID ADD25635 standard; protein; 189 AA.

XX ADD25635;
 AC ADD25635;
 DT 15-JAN-2004 (first entry)
 XX Binding domain-immunoglobulin fusion protein-associated protein #95.
 DE Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX Unidentified.
 OS US2003118592-A1.
 XX 26-JUN-2003.
 XX 25-JUL-2002; 2002US-00207655.
 XX 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX (GENE-) GENE-CRAFT INC.
 XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 PI

QY 131 CWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169
Db 785 CWIGLRNNSGWRWEDGSPLNFSRTNGTIIIRKXHLHKN 823

RESULT 5
ID AAE11760 standard; protein; 188 AA.
AC AAE11760;
XX 18-DEC-2001 (first entry)
XX Mouse mast cell function associated antigen (MAFA) protein.
XX Mouse; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 64..188
FT /note= "Extracellular domain"
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Mikayama T;
PI WPI; 2001-611482/70.
XX
XX N-PSDB; AAD18735.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
XX Sequence 188 AA;

Query Match 53.6%; Score 548.5; DB 4; Length 188;
Best Local Similarity 55.6%; Pred. No. 6.7e-49;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPQVDSEKWLKAVLHRPHLSRFAMVALGLTIVILMSLLYQRL 60

QY 131 CWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169
Db 785 CWIGLRNNSGWRWEDGSPLNFSRTNGTIIIRKXHLHKN 823

RESULT 6
ID AAR77033 standard; protein; 188 AA.
XX
AC AAR77033;
XX
DT 01-FEB-1996 (first entry)
XX
XX Mammalian mast cell function-associated antigen (MAFA).
XX
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
XX
XX Rattus rattus.
XX
XX WO9527734-A1.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1995; 95WO-US004258.
XX
XX 08-APR-1994; 94IL-00109257.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX (RYCU/) RYCU A.
XX
XX Pecht I, Guthmann MD, Tal M;
XX
XX WPI; 1995-366356/47.
XX
XX N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
XX Claim 12; Page 37; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
XX Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPRVQDDSRWKVAVLHRPCVSLVMVALGLTIVILMSLLYQRTL 60

QY 61 CGGSNYTSCPCSPDRWMKYGNHCYFYSVEEKDWNSLLEFCLARDSHLLVITDQEMS 120
Db 61 CGSGKGFMCSCQCRNPLWNRNGSHCYFYSMEKRDWNSLKFCDKGSLLTFFPDNQGVN 120

QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKGLQASCEVPL 180
Db 121 LFGYLGQDFYWIGLRNIDGWRWEGPALSL-RILTNSLIQRCGAHNRNGLQASCEVAL 179

QY 181 HGVCKKV 187
Db 180 QWICKV 186

QY 61 CGGSNYTSCPCSPDRWMKYGNHCYFYSVEEKDWNSLLEFCLARDSHLLVITDQEMS 120
Db 61 CGSGKSTCHPCSPILWTNGSHCYFYSMEKDWNSLKFCDKGSLLTFFPDNQGVK 120

QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKGLQASCEVPL 180
Db 121 LFGYLGQDFYWIGLRNIDGWRWEGPALSL-RILTNSLIQRCGAHNRNGLQASCEVAL 179

QY 181 HGVCKKV 187
Db 180 QWICKV 186

RESULT 6
ID AAR77033 standard; protein; 188 AA.
XX
AC AAR77033;
XX
DT 01-FEB-1996 (first entry)
XX
XX Mammalian mast cell function-associated antigen (MAFA).
XX
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
XX
XX Rattus rattus.
XX
XX WO9527734-A1.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1995; 95WO-US004258.
XX
XX 08-APR-1994; 94IL-00109257.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX (RYCU/) RYCU A.
XX
XX Pecht I, Guthmann MD, Tal M;
XX
XX WPI; 1995-366356/47.
XX
XX N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
XX Claim 12; Page 37; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
XX Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDSVIYSMLELPTATQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLYQWIL 60
Db 1 MADSSIYSTLELPEAPRVQDDSRWKVAVLHRPCVSLVMVALGLTIVILMSLLYQRTL 60

QY 61 CGGSNYTSCPCSPDRWMKYGNHCYFYSVEEKDWNSLLEFCLARDSHLLVITDQEMS 120
Db 61 CGSGKGFMCSCQCRNPLWNRNGSHCYFYSMEKRDWNSLKFCDKGSLLTFFPDNQGVN 120

QY 121 LLOVFLSEAFQWIGLRNNSGWRWEDGSPLNFSRISSNSFVOTCGAINKGLQASCEVPL 180
Db 121 LFGYLGQDFYWIGLRNIDGWRWEGPALSL-RILTNSLIQRCGAHNRNGLQASCEVAL 179

QY 181 HGVCKKV 187
DB 180 QWICKV 186

RESULT 7
AAW88277

ID AAW88277 standard; protein; 188 AA.
XX
AC AAW88277;
XX
DT 29-MAR-1999 (first entry)
XX
Rat mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; splice variant; rat;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX
Rattus sp.
OS
FH Key Location/Qualifiers
FT Modified-site 82...84
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 97...99
FT Modified-site /note= "Asn is N-glycosylated"
XX
PN W09854209-A2.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-GB001572.
XX
PR 31-MAY-1997; 97GB-00011148.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
PI
DR WPI; 1999-059806/05.
DR N-PSDB; AAW84222.
XX
XX New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.
XX
XX Disclosure; Fig 4; 44pp; English.
XX
XX This is the amino acid sequence of rat mast cell function-associated
XX antigen (MAFA), a type II membrane glycoprotein found on mast cells and
XX basophils. The invention relates to cloning of the human MAFA molecule
XX (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
XX of human MAFA that are not found in rat. Polypeptides and synthetic
XX peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
XX and polynucleotides encoding them, can be used in methods for the
XX treatment of inflammatory and allergic diseases (e.g. rheumatoid
XX arthritis and asthma), and tumour growth
XX
XX Sequence 188 AA;
XX
Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
XX
QY 1 MTDSVLYMLEPTAQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
DB 1 MADNSIYSTLELPAPARVQDDSRWKVKAVLHRPCVSYLVMVALGLTIVLMSLLYQRTL 60
XX
QY 61 CQGSNYSTCASCPCPDWMKYNHCHYFYSVEEDKWNSSLEFCLARDSHLIVITDNCBMS 120
DB 61 CCGSKGFCMCQSCSRCPENLWNRNGSHCYFYSMEKRDWNSSLKFCADKDGSHLITTFPDNOGVN 120

QY 121 LLOVELSEAFCEWGLRNNNSQWREDGSPLENFSLISSNSFVOTCGAINKNGLOASSCEVPL 187
DB 121 LFOYVGEDFYWIGLRDIDGWRWEDGPAULSL-ILSNSVYVQKGTTHRCGLHASSEVAL 179

QY 181 HGVCKKV 187
DB 180 QWICKV 186

RESULT 8
AAE11761

ID AAE11761 standard; protein; 188 AA.
XX
AC AAE11761;
XX
DT 18-DEC-2001 (first entry)
XX
Rat mast cell function associated antigen (MAFA) protein.
XX
KW Rat; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX
OS Rattus norvegicus.
XX
PN W0200170805-A2.
XX
PD 27-SEP-2001.
XX
PF 16-MAR-2001; 2001WO-US008596.
XX
PR 17-MAR-2000; 2000US-0190716P.
XX
PA (GEMI-) GEMINI SCI INC.
XX
PI Takahashi N, Mikayama T;
PI
DR WPI; 2001-611482/70.
DR N-PSDB; AAD18736.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is rat MAFA protein
XX
XX Sequence 188 AA;
XX
Query Match 51.4%; Score 525.5; DB 4; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
XX
QY 1 MTDSVLYMLEPTAQNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
DB 1 MADNSIYSTLELPAPARVQDDSRWKVKAVLHRPCVSYLVMVALGLTIVLMSLLYQRTL 60
XX
QY 61 CQGSNYSTCASCPCPDWMKYNHCHYFYSVEEDKWNSSLEFCLARDSHLIVITDNCBMS 120
DB 61 CCGSKGFCMCQSCSRCPENLWNRNGSHCYFYSMEKRDWNSSLKFCADKDGSHLITTFPDNOGVN 120


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XX 29-MAR-1999 (first entry)
XX Human MAFA splice variant huMAFA(E3-).
XX Mast cell function-associated antigen; MAFA; huMAFA(E3-); splice variant;
XX human; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
XX therapy.
XX Homo sapiens.
XX WO9854209-A2.
XX 03-DEC-1998.
XX 29-MAY-1998; 98WO-GB001572.
XX 31-MAY-1997; 97GB-00011148.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX WPI; 1999-059806/05.
XX N-PSDB; AAV84199.
XX New polypeptide having a sequence corresponding to human mast cell
XX function-associated antigen - useful in forming and manufacturing
XX pharmaceutical compositions in the treatment of inflammatory and allergic
XX diseases, and tumour growth.
XX Disclosure; Fig 2; 44pp; English.
XX This is the amino acid sequence of human mast cell function- associated
XX antigen (MAFA) splice variant huMAFA(E3-). huMAFA(E3-) is a major
XX transcript, not found in rat, but highly expressed in human lung and
XX granulocyte-enriched blood cells. The truncated protein includes the
XX intracellular and transmembrane regions of human MAFA (see AAW88265),
XX followed immediately by a polyproline motif (see AAW88264) due to a
XX reading frameshift. This unique motif has been used to design peptides
XX (see AAW88259-64, AAW88268-72) that inhibit T cell antigen receptor-
XX dependent activation induced by interleukin-2 (IL2) secretion from human
XX Jurkat T cells or IgE dependent degranulation of rat basophil leukaemic
XX cells. Inhibition of IL2 production prevents T cell proliferation and
XX suppresses the immune system. These peptides, truncated MAFA polypeptides
XX including huMAFA(E3-), and polynucleotides encoding them, can be used be
XX used in compositions for the treatment of inflammatory and allergic
XX diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
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XX Sequence 70 AA;
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XX Query Match 30.0%; Score 306.5; DB 2; Length 70;
XX Best Local Similarity 82.9%; Pred. No. 3.5e-24;
XX Matches 63; Conservative 1; Mismatches 5; Indels 7; Gaps 1;
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XX 1 MTDVSIYSMLELPATQAQNDYGPQOKSSSKPSCSCLVAITLGLTAVLLSVLLYQWIL 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 61 CQGSNSTCASCPSCP 76
XX |||||
XX 61 CQ-----EPAPSPFP 69
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XX RESULT 12
XX ABB81897
XX ID ABB81897 standard; protein; 231 AA.
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XX AC ABB81897;
XX
XX DT 03-OCT-2002 (first entry)
XX
XX DE Human NKp80.

```

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XX Human; NKp80; triggering NK; lymphoproliferative diseases; LDGL;
XX lymphocyte.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 24 /note= "Encoded by CAA"
XX Misc-difference 43 /note= "Encoded by ACA"
XX Misc-difference 64 /note= "Encoded by CAG"
XX Misc-difference 158 /note= "Encoded by ATC"
XX
XX EF1219637-A1.
XX 03-JUL-2002.
XX 27-DEC-2000; 2000EP-00403689.
XX 27-DEC-2000; 2000EP-00403689.
XX (INNA-) INNATE PHARMA.
XX (UYGE-) UNIV GENOVA.
XX Moretta A, Bottino C, Biassoni R;
XX WPI; 2002-521944/56.
XX N-PSDB; ABQ78832.
XX
XX New NKp80 polypeptides having a triggering NK activity, useful as markers
XX for typing lymphoproliferative diseases of granular lymphocytes, or for
XX identifying abnormal cells in the whole lymphocyte population in patient.
XX Claim 4; SEQ ID NO 1; 21pp; English.
XX
XX The invention relates to a novel human polypeptide (designated NKp80)
XX having a triggering NK activity, or its immunogenic fragments. The NKp80
XX polypeptide is useful as NK cell markers, as markers for typing
XX lymphoproliferative diseases of granular lymphocytes (LDGL), or for
XX identifying abnormal cells in the whole lymphocyte population of the
XX patient. The antibodies against these polypeptides are useful for
XX inhibiting NK cell cytotoxicity or NK cell depletion. The sequence
XX represents the human NKp80 polypeptide of the invention. N.B. The
XX sequence data for this patent is not represented in the printed
XX specification, but is based on sequence information supplied by the
XX European Patent Office
XX
XX Sequence 231 AA;
XX
XX Query Match 22.5%; Score 230; DB 5; Length 231;
XX Best Local Similarity 28.6%; Pred. No. 1.7e-15;
XX Matches 63; Conservative 32; Mismatches 61; Indels 64; Gaps 9;
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XX 26 QKSSSKPSCSCL--VAITL-----GLLTAVLLSVLLY-----QWILCQG-- 63
XX :|||: ||||| :||| :||| :||| :||| :||| :||| :|||
XX 15 KRSSAQTSCLTFKDYSVTLHWYKILLIGISGTVNGILTLISLLILVSCGVLLKCKGKS 74
XX
XX 64 -----SNYSTCASCPS-----CPDRMKYGNHCYFVSVEKD 95
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XX 75 CSNATQVEDTGLKVNGTFRNINSDLCASRSADQTVLCQSEWLKYQKCYWFSNEMKS 134
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XX 96 WNSSLBFCLARDSHLLVITDNOQMSLLIQVFLSEA-FCWIGLRNNS---GWRWEDGSPLN 151
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XX 135 WSDSYVYVCLERKSHLLIIHQLEMAFIQKNLRQLNYVWIGLNTSLKMTWTWVGSPID- 193
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XX 152 SRISNSFWO-----TCGAINKNGLQASCEVPLHGVCX 185
XX ||||| :||| :||| :||| :||| :||| :||| :|||
XX 194 ---SKIFFIKGPAKENSCAAIKESKIFSETCSSVFKWICQ 230
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RESULT 13
AAM88815
ID AAM88815 standard; protein; 198 AA.
XX AAM88815;
AC AAM88815;
XX AAM88815;
DT 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen SEQ ID NO:16408.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX Homo sapiens.
OS Homo sapiens.
PN WO200157182-A2.
XX WO200157182-A2.
PD 09-AUG-2001.
XX 09-AUG-2001.
PF 17-JAN-2001; 2001WO-US001354.
XX 31-JAN-2000; 2000US-0179065P.
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PR 19-MAY-2000; 2000US-0205515P.
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PR 28-JUN-2000; 2000US-0214886P.
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XX AC ABP48040;
XX DT 23-AUG-2002 (first entry)
XX DE Human polypeptide SEQ ID NO 470.
XX KW Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antischling; antianaemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerobroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN US2002042386-A1.
XX PD 11-APR-2002.
XX PF 17-JAN-2001; 2001US-00764870.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 11-JUL-2000; 2000US-0217496P.
XX PR 16-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
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XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225267P.
XX PR 14-AUG-2000; 2000US-0225268P.
XX PR 14-AUG-2000; 2000US-0225270P.
XX PR 14-AUG-2000; 2000US-0225447P.
XX PR 14-AUG-2000; 2000US-0225757P.
XX PR 22-AUG-2000; 2000US-0225758P.
XX PR 30-AUG-2000; 2000US-0228924P.
XX PR 01-SEP-2000; 2000US-0229287P.
XX PR 01-SEP-2000; 2000US-0229343P.
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XX PR 17-NOV-2000; 2000US-0249299P.
XX PR 08-DEC-2000; 2000US-0251856P.
XX PR 08-DEC-2000; 2000US-0251868P.
XX PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2002-470713/50.
DR N-PSDB; ABQ66715.
XX New nucleic acid encoding human proteins, useful for diagnosis, treatment
PT and prevention of e.g. osteoporosis, also related polypeptides and
PT antibodies.
XX Claim 11; SEQ ID NO 470; 235pp + Sequence Listing; English.
XX The invention relates to novel genes (ABQ66521-ABQ66785) and proteins
CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?docid=999909764870
XX SQ Sequence 198 AA;
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Best Local Similarity 31.2%; Pred. No. 3.5e-15;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-811-367B-1

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1007	98.4	189	14 US-10-207-655-196	Sequence 196, App
3	548.5	53.6	188	9 US-09-811-367B-3	Sequence 3, Appli
4	525.5	51.4	188	9 US-09-811-367B-5	Sequence 5, Appli
5	230	22.5	231	16 US-10-451-843-1	Sequence 1, Appli
6	226	22.1	198	9 US-09-764-870-470	Sequence 470, App
7	226	22.1	198	14 US-10-125-540-470	Sequence 470, App
8	226	22.1	203	9 US-09-764-870-309	Sequence 309, App
9	226	22.1	203	14 US-10-125-540-309	Sequence 309, App
10	217	21.2	35	9 US-09-864-761-33902	Sequence 33902, A
11	216.5	21.2	182	9 US-09-764-870-310	Sequence 310, App
12	216.5	21.2	182	14 US-10-125-540-310	Sequence 310, App
13	201	19.6	225	15 US-10-379-127-25	Sequence 25, Appl
14	196.5	19.2	179	10 US-09-919-039-130	Sequence 130, App
15	196.5	19.2	179	15 US-10-335-009-10	Sequence 10, Appli

16	196.5	19.2	199	14	US-10-179-528-7	Sequence 7, Appli
17	195.5	19.1	278	14	US-10-220-511-11	Sequence 11, Appl
18	194	19.0	268	15	US-10-161-493-22	Sequence 22, Appl
19	193.5	18.9	226	14	US-10-002-631C-295	Sequence 295, App
20	193	18.9	257	14	US-10-179-528-4	Sequence 4, Appli
21	193	18.9	270	14	US-10-220-511-4	Sequence 4, Appli
22	190	18.6	265	9	US-09-764-870-307	Sequence 307, App
23	190	18.6	285	14	US-10-125-540-307	Sequence 307, App
24	189.5	18.5	275	15	US-10-161-493-20	Sequence 20, Appl
25	187	18.3	399	16	US-10-451-459-2	Sequence 2, Appli
26	185.5	18.1	316	9	US-09-862-802-4	Sequence 4, Appli
27	183	17.9	319	15	US-10-138-588-90	Sequence 90, Appl
28	182	17.8	216	15	US-10-335-009-8	Sequence 8, Appli
29	181	17.7	273	9	US-09-796-858-47	Sequence 47, Appl
30	181	17.7	273	14	US-10-220-511-2	Sequence 2, Appli
31	180.5	17.6	546	12	US-10-072-012-158	Sequence 158, App
32	180.5	17.6	549	12	US-10-072-012-160	Sequence 160, App
33	180	17.6	223	12	US-10-276-774-2216	Sequence 2216, Ap
34	179.5	17.5	273	9	US-09-862-802-10	Sequence 10, Appl
35	179	17.5	267	15	US-10-138-588-88	Sequence 88, Appl
36	178	17.4	345	12	US-10-262-839-94	Sequence 94, Appl
37	176	17.2	404	10	US-09-891-894-1	Sequence 1, Appli
38	176	17.2	404	12	US-10-151-274-2	Sequence 2, Appli
39	176	17.2	404	14	US-10-184-150-1	Sequence 1, Appli
40	176	17.2	404	15	US-10-369-214-131	Sequence 131, App
41	176	17.2	404	15	US-10-328-997-1	Sequence 1, Appli
42	175	17.1	149	10	US-09-284-320-11	Sequence 11, Appl
43	175	17.1	149	13	US-10-114-893-32	Sequence 32, Appl
44	175	17.1	149	14	US-10-088-859-2	Sequence 2, Appli
45	175	17.1	149	14	US-10-179-528-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No, US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1

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Best Local Similarity 100.0%; Pred.No 3.5e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	COGSNTSCASCPDRCRWKYNHCYFVSVEBKDNSSLEFCLARDSHLLVITDQEMS 120
DB	61	COGSNTSCASCPDRCRWKYNHCYFVSVEBKDNSSLEFCLARDSHLLVITDQEMS 120
QY	121	LLOVFLSEAFCTGLRNNSWRWEDGSPNFRISNSFVOTCGATKNGKQASSCEVPL 180
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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-843-1

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Best Local Similarity 28.6%; Pred. No. 2.5e-15;
Matches 63; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

QY 26 QKSSSKSPSCSL--VAITL-----GLLTAVLLSVLLY---QWILCOG-- 63
Db 15 KKRSSAGTSCLTFKDYSVTLHWYKILLIGISGTNGILTLISLILVSGVLLKCKGKS 74
QY 64 -----SNYSTCASCPS-----CPDRMKYGNHCYFVSVEEKD 95
Db 75 CSNATQYEDTGLKVNNGTRRNISNKCDCASRSADQTVLCQSEWLKYQKCYWFSNEMKS 134
QY 96 WNSLEPCLARDSHLLVITDQEMSLLOVFLSEA-FCWIGLRNNS-----GWRWEDGSPINF 151
Db 135 WSDSYVYVCLERKSHLLIHDQLEMAFIQKNLRQLNLYWVIGLFTSLKMTWTWVDGSPID- 193
QY 152 SRISSNSFVQ-----TCGAINKNGLOASSCEVPLHGVCK 185
Db 194 ---SKIFFIKGPAKENSAAIKESKIFSETCSSVFVKWICQ 230

RESULT 6
US-09-764-870-470
; Sequence 470, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 470
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-470

Query Match      22.1%; Score 226; DB 9; Length 198;
Best Local Similarity 31.2%; Pred. No. 5.4e-15;
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

QY 44 GLLTAVLLSVLLY--QWIL--COG-----SNYSTCASCPS 74
Db 16 GILTLTILISLILVSGVLLKCKQKGCSCNATQYEDTGLKVNNGTRRNISNKCDCASRSA 75
QY 75 -----CPDRMKYGNHCYFVSVEEKDWSLEFCLARDSHLLVITDQEMSLLOVFLSEA 129
Db 76 DQTVLCQSEWLKYQKCYWFSNEMKSWSDSYVYVCLERKSHLLIHDQLEMAFIQKNLRQL 135
QY 130 -FCWIGLRNNS---GWRWEDGSPINFSRISNSFVQ-----TCGAINKNGLOASSCEVP 179
Db 136 NYVMVIGLFTSLKMTWTWVDGSPID---SKIFFIKGPAKENSAAIKESKIFSETCSSV 191
QY 180 LHGVCK 185
Db 192 FWKICQ 197

RESULT 7
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; Sequence 309, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 309
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-309

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Best Local Similarity 31.2%; Pred. No. 5.5e-15;
Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

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QY 130 -FCWIGLRNNS---GWRWEDGSPINFSRISNSFVQ-----TCGAINKNGLOASSCEVP 179
Db 141 NYVMVIGLFTSLKMTWTWVDGSPID---SKIFFIKGPAKENSAAIKESKIFSETCSSV 196
QY 180 LHGVCK 185
Db 192 FWKICQ 197

US-10-125-540-470
; Sequence 470, Application US/10125540
; Publication No. US20030059875A1
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; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match      19.2%; Score 196.5; DB 15; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

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Qy      93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFCWIGL--RNNSGWRWEDGSPL 149
Db      79 QKTWNEERHLCAQXSSLLQONTDELDFMS--SSQQFYWIGLSYSEHTAWLWENGSA 136
Qy      150 NFSRISSNSF----VQTGAINKNG-LOASSCEVELHGVCKK 186
Db      137 --SOVLFPSTFTNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
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Job time : 41.4761 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.7186 Seconds
(without alignments)
662.924 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLELTATQAQN.....GLQASCEVPLHGVCCKVRL 189

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	201	19.6	225	2	US-08-738-462-2
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8	196.5	19.2	179	1	US-08-690-095-9
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11	196.5	19.2	179	2	US-09-113-788-3
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13	196.5	19.2	199	5	PCT-US93-10418-4
14	193	18.9	270	2	US-09-055-095-4
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16	193	18.9	270	3	US-09-352-302-2
17	193	18.9	273	2	US-08-809-494A-4
18	193	18.9	273	3	US-09-352-302-4
19	190	18.6	233	1	US-08-690-095-8
20	190	18.6	233	3	US-09-113-789-8
21	190	18.6	233	3	US-08-543-246B-2
22	190	18.6	233	3	US-08-543-246B-21
23	185.5	18.1	316	3	US-09-111-470-4
24	184	18.0	215	1	US-08-690-095-7
25	184	18.0	215	3	US-09-113-789-7
26	184	18.0	215	3	US-08-543-246B-16
27	184	18.0	215	3	US-08-543-246B-22

28 182 17.8 231 1 US-08-690-095-6 Sequence 6, Appli
29 182 17.8 231 3 US-09-113-789-6 Sequence 6, Appli
30 182 17.8 231 3 US-08-543-246B-6 Sequence 6, Appli
31 182 17.8 231 3 US-08-543-246B-23 Sequence 23, Appli
32 181 17.7 273 2 US-09-055-095-3 Sequence 3, Appli
33 181 17.7 273 2 US-08-809-494A-6 Sequence 6, Appli
34 181 17.7 273 3 US-09-352-302-6 Sequence 6, Appli
35 180 17.6 216 3 US-08-543-246B-9 Sequence 9, Appli
36 180 17.6 216 3 US-08-543-246B-24 Sequence 24, Appli
37 179.5 17.5 273 3 US-09-111-470-10 Sequence 10, Appli
38 179.5 17.5 292 2 US-08-688-342-4 Sequence 4, Appli
39 179.5 17.5 292 2 US-09-113-788-4 Sequence 2, Appli
40 176 17.2 404 4 US-09-517-605-2 Sequence 17, Appli
41 175.5 17.2 168 3 US-08-772-440-17 Sequence 1, Appli
42 175.5 17.2 201 2 US-08-688-342-1 Sequence 1, Appli
43 175.5 17.2 201 2 US-09-113-788-1 Sequence 2, Appli
44 174 17.0 199 5 PCT-US93-10418-2 Sequence 2, Appli
45 173 16.9 175 3 US-08-772-440-15 Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5
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Best Local Similarity 53.5%; Pred. No. 1.1e-48;

Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
QY 1 MTDSVIYMLELPTAQNNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLTTLVILMSLLDYQRTL 60
QY 61 CQGSNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMS 120
Db 61 CQSGKGFMCSCRCPLWNRNGSHCYFVSMEKRDWNSSLKFCADKGSLLTFFPDQGVN 120
QY 121 LLQVFLSEAPCWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASCEVPL 180
Db 121 LFQEVGVGDFYWIGLRIDGWRWEDGPALSLS-ILSNSVWQKGTIHRCGLHASCEVAL 179
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Db 180 QWICEKV 186

RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT: BROWDY AND NEIMARK
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-5

Query Match 51.4%; Score 525.5; DB 5; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
QY 1 MTDSVIYMLELPTAQNNDYGPQOKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLTTLVILMSLLDYQRTL 60
QY 61 CQGSNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMS 120
Db 61 CQSGKGFMCSCRCPLWNRNGSHCYFVSMEKRDWNSSLKFCADKGSLLTFFPDQGVN 120

QY 121 LLQVFLSEAPCWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASCEVPL 180
Db 121 LFQEVGVGDFYWIGLRIDGWRWEDGPALSLS-ILSNSVWQKGTIHRCGLHASCEVAL 179
QY 181 HGVCKKV 187
Db 180 QWICEKV 186
RESULT 3
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531.056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
Query Match 42.0%; Score 430; DB 4; Length 76;
Best Local Similarity 98.7%; Pred. No. 6e-39;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 PSCPDWRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDQEMSLLQVFLSEAFW 60
QY 133 IGLRNSGWRWEDGSP 148
Db 61 IGLRNSGWRWEDGSP 76

RESULT 4
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722.126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257

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; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PCHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-6

Query Match 36.2%; Score 370.5; DB 3; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

Qy 75 CPDRWMKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFQWIG 134
Db 1 CPNLWMNGSCHYFYSMEKEDWNSLKFCDKGSLLTTFDNGQVNLFOEYVGDFYWG 60

Qy 135 LRNSGWRWEDGSPNFSRISNSFVOTCGAINKNGLOASSCEVPLHGVCVKV 187
Db 61 LRIDGWRWEDGPALSLS-ILNSNVQKGTIHRGGLHASSCEVALQWICEKV 112

RESULT 5
PCT-US95-04258-6
; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PCHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-6

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Query Match 36.2%; Score 370.5; DB 5; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

Qy 75 CPDRWMKYGNHCYFYSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFQWIG 134
Db 1 CPNLWMNGSCHYFYSMEKEDWNSLKFCDKGSLLTTFDNGQVNLFOEYVGDFYWG 60

Qy 135 LRNSGWRWEDGSPNFSRISNSFVOTCGAINKNGLOASSCEVPLHGVCVKV 187
Db 61 LRIDGWRWEDGPALSLS-ILNSNVQKGTIHRGGLHASSCEVALQWICEKV 112

RESULT 6
US-08-738-462-2
; Sequence 2, Application US/08738462
; Patent No. 5965401
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Lanier, Lewis L.
; APPLICANT: Phillips Jr., Joseph H.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; RELATED REAGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,462
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,435
; FILING DATE: 16-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Chang, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0397
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-738-462-2

Query Match 19.6%; Score 201; DB 2; Length 225;
Best Local Similarity 26.0%; Pred. No. 1.1e-13;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

Qy 1 MTDSVIYSMLPTATQANDYGFQKSSSSKP-----SCSCLVAITLG 44
Db 1 MDQQAIAELNLT-----DSGPSSSPSLPRDVCQSPWHQFALKSCAGILLVL- 53

Qy 45 LTTAVLLSVLLYQWILLCOGNSYSTCA-----SCSPCDRWKMYGNHCYFYS 90
Db 54 VVTGLSVSVT-----SLIQKSSIEKCSVDIQQSRNKTKTERPGLNCPITYWQOLREKCLLFS 109

Qy 91 VEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSE--AFQWIGLR---NNSGWRWED 145
Db 110 HTVNPWNNSLADCTKESLLLRDDELHHTQNLIRDKAILFWGLNFSLSKKNWKNIN 169

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QY 146 GSPNFS--RISNSFVOTCGAINKNGLOASSCEVPLHGVCCK 186
Db 170 GSFLNSDLIRGDAKENSICISQTSVSYEVCSTEIRWICQK 212

RESULT 7

PCT-US94-07587-2
; Sequence 2, Application PC/TUS9407587
; GENERAL INFORMATION:
; APPLICANT: Schering Corp.
; TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering Corp.
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07587
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: DX0397K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7255
; TELEFAX: 201-822-7039
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07587-2

Query Match 19.6%; Score 201; DB 5; Length 225;
Best Local Similarity 26.0%; Pred. No. 1.1e-13;
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDVIYSMLPTATQAQNDYGPQKSGSSXK-----SCSLVAITIG 44
Db 1 MDQQAIVAEALNLP-----DSGPSSSPSSLPDRVCOGSPWHQFALKSCAGIILLVL- 53
QY 45 LTAVALLSVLLYQWTLCOGSNVTCA-----SCPSCPDRMKYGNHCYFVS 90
Db 54 VVTGLSVSVT-----SLIOKSSIEKGSVDIQSRNKTTPRGLLNCPIYQQLRKCLLFS 109
QY 91 VEEKDWSLEFLCARDHLAVITDNCMSLLQVFLSE--AFCWIGLR---NNSGWRWED 145
Db 110 HTVNPWNNSLADCSKESLLIRDKDELHTQNLIRKAILFGLNFSLEKNKWKIN 169
QY 146 GSPNFS--RISNSFVOTCGAINKNGLOASSCEVPLHGVCCK 186
Db 170 GSFLNSDLIRGDAKENSICISQTSVSYEVCSTEIRWICQK 212

RESULT 8

US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-08-690-095-9

Query Match 19.2%; Score 196.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSQLVAITIGLITAVLLSVLLYQWTLCOGSN--YSTCASCPCSPDRMKYGNHCYFVSVE 92
Db 20 CILSMA-TLGIILKNSFTKLSIEPAFTPGPNIELQKSDCCSQCKWGYRCNCYFISSE 78
QY 93 EKWNSSLEFLCARDHLAVITDNCMSLLQVFLSEAFCWIGL---RNSGWRWEDGSPL 149
Db 79 QRTWNSRHLCASQSSLLQNTDELDFMS--SSQFYWIGLSYSEEHATWENGSA 136
QY 150 NPSRISSNSF----VQTGAINKNG-LOASSCEVPLHGVCCK 186
Db 137 --SQVLFPSFEFTFKNCIAYNPNGNALDESCEDKNRYICKQ 176

RESULT 9

US-08-650-578-2
; Sequence 2, Application US/08650578
; Patent No. 5811284
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Aramburu Beltran, Jose
; APPLICANT: Lopez-Botet, Miguel
; APPLICANT: Phillips Jr., Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA


```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
US-09-113-788-3

Query Match          19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNHCYFVSVE 92
Db 20 CLSLMA-TLGLLLKNSFTKLSIEPAFTGPNIELQKSDCCSCQEKWGYRCNCYFISSE 78

QY 93 EKDNSSLEFCLARDSHLVTIDNQEMSLLOVFISEAFMWGL---RNNSGWRWEDGSPL 149
Db 79 QKTWNERHLCAQKSSLLQNTDQLDFMS--SSQQFYWIGLSYSEHTAWLWENGSA 136

QY 150 NFSRISSNSP----VOTCGAINKNG-LOASCEVPLHGVCKK 186
Db 137 --SQYLPSPFTFTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

RESULT 12
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-09-113-789-9

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
US-09-113-788-3

Query Match          19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNHCYFVSVE 92
Db 20 CLSLMA-TLGLLLKNSFTKLSIEPAFTGPNIELQKSDCCSCQEKWGYRCNCYFISSE 78

QY 93 EKDNSSLEFCLARDSHLVTIDNQEMSLLOVFISEAFMWGL---RNNSGWRWEDGSPL 149
Db 79 QKTWNERHLCAQKSSLLQNTDQLDFMS--SSQQFYWIGLSYSEHTAWLWENGSA 136

QY 150 NFSRISSNSP----VOTCGAINKNG-LOASCEVPLHGVCKK 186
Db 137 --SQYLPSPFTFTKNCIAYNPNGNALDESCEDKKNRYICKQ 176

RESULT 13
PCT-US93-10418-4
; Sequence 4, Application PC/TUS9310418
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Hjerrild, Kathryn A.
; TITLE OF INVENTION: Activation Antigen CD69
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10418
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2610-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-10418-4

Query Match          19.2%; Score 196.5; DB 5; Length 199;
Best Local Similarity 27.2%; Pred. No. 2.7e-13;
Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;

QY 17 QAQNDYGPQ---QKSSSSKPCSCLVAILTGLLTAVLLSVLLYQWILCOGSNYSTCASC 73
Db 18 RGQKDHGTSHFPEKHGEG---SIQVSIPIWAVLIVLITSLITLIALNLVNGKY----NCP 69

QY 74 -----SCPDWMKYGNHCYFVSVEEKDNSSLEFCLARDSHLVTIDNQEM 119
Db 70 GLYEKLESSDHHVATCKNEWISYKRTCYFFSTTKSWALAQSSCEDARTLAVIDSEKDM 129

QY 120 SILQVFISEAFMWGLRN--NSGWRWEDGSPLN--FSRISNSFVQTGAINKNGLOASS 175
Db 130 TFLKRYSGELEHWIGLKNEANQTKWANGKFNFWNLTGSG----RCVSVNHKNVTAYD 185

QY 176 CEVPLHGVCKK 186
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Db      186 CEANFWVCSK 196
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RESULT 14
US-09-055-095-4
; Sequence 4, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1902982
US-09-055-095-4

Query Match      18.9%; Score 193; DB 2; Length 270;
Best Local Similarity 30.6%; Pred. No. 9.8e-13;
Matches 44; Conservative 25; Mismatches 53; Indels 22; Gaps 5;

QY      57 QWILCOGSNYSTCASCPCDRMKYGNHCYFVSVEKDWNSLSEFCCLARDSHLLVITDN 116
Db      127 QEVLEKAANY-----GPCPDWLWHEENCYQFSSGSFNWKSQENCLSLDAHLKINST 181

QY      117 QEMSLQVFLSEAF--CWIGL---RNSGWRWEDGSPLN-----FSRISNSFVQT 162
Db      182 DELEFIQOMIAHSSFPFWMLSMRKPNYSWLWEDGTPLTFLPRIQGAVERMYPSG---T 238

QY      163 CGAINKNGLOASSCEVPLHGVCVK 186
Db      239 CAYIQGTVEAENCILTAFSICQK 262

Search completed: August 10, 2004, 16:20:31
Job time : 15.7186 secs

Db      186 CEANFWVCSK 196
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RESULT 15
US-08-809-494A-2
; Sequence 2, Application US/08809494A
; Patent No. 5962260
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 11.9788 Seconds
(without alignments)
1509.673 Million cell updates/sec

Title: US-09-811-367B-3
Perfect score: 1029
Sequence: 1 MADSSYSTLELPEAPQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	81.4	198	2 I59421	mast cell function
2	182	17.7	257	2 I50146	gene 17.5 protein
3	180.5	17.5	227	2 A46467	natural killer cell
4	173.5	16.9	199	2 JH0822	lymphocyte early a
5	164.5	16.0	225	2 J38700	hNKR-P1a protein -
6	163.5	15.9	146	2 JC7135	agkisacutacin beta
7	160.5	15.6	231	2 PT0374	natural killer cell
8	155.5	15.1	156	2 T28141	C type lectin, B 1
9	152.5	14.8	146	2 JC4691	coagulation factor
10	152.5	14.8	1479	2 T42710	mannose receptor,
11	151	14.7	233	2 PT0372	natural killer cell
12	151	14.7	1487	2 S48719	phospholipase-A(2)
13	149	14.5	223	2 E46457	NKR-P1 protein hom
14	149	14.5	404	2 A46274	HIV gp120-binding
15	147.5	14.3	359	2 A43532	aggreitin beta chain
16	146.5	14.2	146	2 JC7105	NK-cell receptor p
17	146.5	14.2	223	2 A35917	NKR-P1 protein hom
18	146	14.2	220	2 C46467	natural killer cell
19	144	14.0	216	2 PT0375	natural killer cell
20	144	14.0	240	2 I54524	natural killer cell
21	144	14.0	301	2 S13165	asialoglycoprotein
22	143.5	13.9	742	2 JC7595	scavenger receptor
23	142	13.8	301	1 LNRT2	hepatic lectin-2 -
24	139	13.5	304	2 JX0209	lectin, galactose/
25	138	13.4	167	1 WNVZ82	hepatic lectin hom
26	136.5	13.3	170	2 T28140	natural killer cell
27	135	13.1	144	2 PC7027	aggreitin alpha cha
28	133	12.9	311	1 LNHT2A	asialoglycoprotein
29	132.5	12.9	1326	2 B56395	secretory phosphol

30 132.5 12.9 1465 2 A56395 secretory phosphol
31 128 12.4 284 2 S29855 asialoglycoprotein
32 128 12.4 550 2 A28166 Kupffer cell recep
33 127.5 12.4 291 1 LNHT1 hepatic lectin H1
34 127 12.3 207 1 LNCHL hepatic lectin - c
35 126 12.2 284 1 LNRTL hepatic lectin - r
36 123 12.0 2124 2 A28452 proteoglycan core
37 122.5 11.9 1463 2 A53210 phospholipase A2 r
38 122 11.9 1458 1 A49707 phospholipase A2 r
39 122 11.9 2132 1 A55182 aggreican precursor
40 121.5 11.8 306 2 A42230 lectin M-ASGP-BP p
41 120.5 11.7 262 2 A30573 T-cell surface gly
42 119.5 11.6 260 2 I49049 Ly-49D-GE antigen
43 119 11.6 133 2 A47267 botroctetin alpha c
44 118.5 11.5 323 1 S09702 L-selectin precurs
45 118.5 11.5 385 1 A34015 L-selectin precurs

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C:Genetics:
A:Gene: mafa

Query Match 81.4%; Score 838; DB 2; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.3e-74;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSYSTLELPEAPQVQDESWKIKAVLHRRPHLSRPFAMVALGLLTIVILMSLLMYQRI 60
Db 1 MADNSYSTLELPAAPKPVQDSRWKVKAVLHRRPCVYLVNVALGLLTIVILMSLLYQRTL 60
Qy 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFFGMEKKDWNSSLKFCADKGSLLTTFPDNGVK 120
Db 61 CCGSGFMCSCQSCPCPNLWNRNGSHCYFFGMEKKDWNSSLKFCADKGSLLTTFPDNGVN 120
Qy 121 LFGYEGQDPYWTGLRNIDGWRWEGGPAISLRILTSIORCGAIHNRNGIQASCEVALQ 180
Db 121 LFGYEVGEDFYWTGLRIDGWRWEDGPAISLSILNSVQKCGTHRCGLHASSCEVALQ 180
Qy 181 WICKKVL 187
Db 181 WICKKVL 187

RESULT 2

I50146
gene 17.5 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50146
R;Bernot, A.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 221-229, 1994
A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc gene:
A:Reference number: I50146; MUID:94164691; PMID:8119728
A:Accession: I50146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

QY 164 AIHRNGLOASSCEVALQWICK 185
Db 175 FLXNTEVSSMECKNLYWICNK 196

RESULT 5
I38700
NKR-P1a protein - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C/Accession: I38700
R/Lanier, L.L.; Chang, C.; Phillips, J.H.
J. Immunol. 153, 2417-2428, 1994
A/Title: Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin superfamily ex
A/Reference number: I38700; MUID:94358407; PMID:8077657
A/Accession: I38700
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-225 <RES>
A/Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PID:9544496
C/Suprafamily: Natural killer cell receptor P1; C-type lectin homology
F/94-210/Domain: C-type lectin homology <LCH>

Query Match 16.0%; Score 164.5; DB 2; Length 225;
Best Local Similarity 27.4%; Pred. No. 1.3e-08;
Matches 60; Conservative 32; Mismatches 90; Indels 37; Gaps 10;

QY 1 MADSSITYSTLELP--EAPQ-----YQDESRLKAKVLRHRLPHLSRFAMVALGL--- 45
Db 1 MDQQAIVAEINLPDTSQSPSSSPULPRDVCQSPWHQFAL----KLSACGIIILLVLVVT 56

QY 46 -LTVILMSLLMYORILCCG-----SKDSTCSH--CPSPCILWTRNGSHCYFYSMEKKDWN 97
Db 57 GLSVSVTSLLQKSIKSCSDVIOQSRNKTTERPGLNLCPIYWOQLREKXCLLFSHTVNPWN 116

QY 98 SSLKFCADKGSLLTTPDNQGVKLFGEYLQD---FYWIGLR---NIDGWRWEGGPALS- 150
Db 117 NSLADGSKSSLLLRDKDEL-IHTQNLIRDKALFELWIGLNSLSEKNWKWNGSPFNS 175

QY 151 --LRILNTSLIORCGAIHRNGLOASSCEVALQWICKKVL 187
Db 176 NDLERGDAKENSICISISQTSVYSEYCSTEIRWICQKEL 214

RESULT 6
JC7135
agkisacutacin beta chain precursor - sharp-nosed viper
N/Alternate names: fibrinogenolytic venom protein
C/Species: Agkistrodon acutus (sharp-nosed viper)
C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C/Accession: JC7135; PC7038
R/Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A/Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A/Reference number: JC7134; MUID:20025379; PMID:10558903
A/Accession: JC7135
A/Molecule type: mRNA
A/Residues: 1-146 <CHE>
A/Cross-references: GB:AF176421
A/Experimental source: venom gland
A/Accession: PC7038
A/Molecule type: protein
A/Residues: 24-50;59-83;102-107;112-114 <CH2>
C/Suprafamily: tetranectin; C-type lectin homology
C/Keywords: disulfide bond; heterodimer; venom
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-146/Product: agkisacutacin beta chain #status experimental <MAT>

Query Match 15.9%; Score 163.5; DB 2; Length 146;
Best Local Similarity 30.2%; Pred. No. 1e-08;
Matches 48; Conservative 15; Mismatches 71; Indels 25; Gaps 6;

QY 35 LSRFAMVALGLTLTVILMSLLMYORILCCGSKDSTCSHCPSPILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSFGLLVFL-----SLSGTAADCPs---EWSSEHGCHYKPFDEPK 44

QY 95 DMNSSLKFCAD--KGSLLTTPDNQGVKLFGEYLQDQFYWIGLRNI-DG--NRWEG 145
Db 45 TWADAEEKFCTQOHKGSLSLASFHSSEADFFVITLTSKLTDLVWIGLKNWNGCYMKWSD 104

QY 146 GPALSRLITNSLIQRCGAIHRNGLOASSCEVALQWICK 184
Db 105 GTKLDYKDWREQECVLSRVTVNNNEWLSMDGTTCSFVCK 143

RESULT 7
PT0374
natural killer cell receptor group 2-C, splice form 1 - human
N/Alternate names: NKG-C
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
C/Accession: PT0374
R/Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A/Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I:
A/Reference number: PT0372; MUID:91178434; PMID:2007850
A/Accession: PT0374
A/Molecule type: mRNA
A/Residues: 1-231 <HOU>
A/Cross-references: EMBL:X54869; NID:935060; PIDN:CAA38651.1; PID:935061
A/Experimental source: natural killer cell
C/Genetics:
A/Gene: GDB:KLC2; NKG2-C
A/Cross-references: GDB:9787095
A/Map position: 12p13-12p13
C/Suprafamily: natural killer cell receptor P1; C-type lectin homology
C/Keywords: glycoprotein; transmembrane protein
F/71-96/Domain: transmembrane #status predicted <TRA>
F/27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.6%; Score 160.5; DB 2; Length 231;
Best Local Similarity 24.4%; Pred. No. 3.3e-08;
Matches 41; Conservative 29; Mismatches 83; Indels 15; Gaps 5;

QY 33 PHLSRFAMVALGLTLTVILMSLLMYORIL-----CCGSKDSTCSHCPSPILWTRNG 83
Db 66 PPEKLTAEVLGICIVLWATVLTIVLPFLQNNSSNPNRTQKARHCHGCFEWTYS 125

QY 84 SHCYFYSMEKKDWNSSILKFCADKGSLLTTPDNQGVKLFGEYLQDQFYWIGLR-RNIDGWR 142
Db 126 NSCYIICKERTWEESILLACTSKNSLLSIDNEEIKFLASILPSS--WIGVFRNSSHP 183

QY 143 WE--GGPALSLRLITNSLIQ-RCGAIHRNGLOASSCEVALQWICKKVL 187
Db 184 WVTINGLAFKHKIKDSDNAELNCALQVNLKSAQCQSGSMIYCHKHL 231

RESULT 8
T28141
C type lectin, B locus - chicken
C/Species: Gallus gallus (chicken)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T28141
R/Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A/Description: DNA sequencing and analysis of the chicken major histocompatibility comp.
A/Reference number: Z20475
A/Accession: T28141
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-156 <MIL>
A/Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A/Experimental source: clone cB12
C/Genetics:
A/Gene: Blec

A;Title: Identification of a human protein homologous to the mouse Lyb-2 B cell differer
A;Reference number: A43532; MUID:90278102; PMID:2141045
A;Accession: A43532
A;Molecule type: mRNA
A;Residues: 1-359 <VON>
A;Cross-references: GB:M54992; NID:g187262; PIDN:AAA36189.1; PID:g187263
C;Genetics:
A;Gene: GDB:CD72
A;Cross-references: GDB:128153; OMIM:107272
A;Map position: 9p-9p
C;Superfamily: C-type lectin homology
C;Keywords: B-cell; glycoprotein; homodimer; surface antigen; transmembrane protein
F;1-95/Domain: intracellular #status predicted <CYT>
F;96-116/Domain: transmembrane #status predicted <TM>
F;117-359/Domain: extracellular #status predicted <EXT>
F;136/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 147.5; DB 2; Length 359;
Best Local Similarity 27.3%; Pred. No. 9.7e-07;
Matches 38; Conservative 19; Mismatches 61; Indels 21; Gaps 6;

QY 62 CGSKDSTCSHCPCFLLWTRNGSHCYFSEMEKDWNSLKFCADKGSLLTF----PDNQ 117
||| ||| ||| ||| : ||| : ||| ||| ||| ||| :
Db 226 CGSAD-TC-----CPSGWIMQKSCFYISLTSKNQESQKQCE TLSSKLATFSEIYPOSH 279
||| ||| ||| ||| : ||| : ||| ||| ||| ||| :
QY 118 GVKLFGELY----GQDFYIWIGLRNIDGWRWEGGPALSLRLITNSLIQRCGAIHRN----G 169
| : ||| : : : : : : : : : : : : : : : :
Db 280 SYFNLNLLPNGSGNSYWTGLSSNKDWKLTDD---TQRTTYAGSSKCKVKHTWSWWT 336
| : ||| : : : : : : : : : : : : : : : :
QY 170 LQASSCEVALQWICKKVLV 188
| : ||| : : : : : : : : : : : : : : : :
Db 337 LESESCRSSLPYICEMTAF 355
| : ||| : : : : : : : : : : : : : : : :

Search completed: August 10, 2004, 16:19:36
Job time : 12.9788 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:41 ; Search time 7.32035 Seconds
(without alignments)
1337.256 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSIVSTLELPEAPQVQD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	180.5	17.5	179	1	Q9mzk9 macaca mula
2	180.5	17.5	227	1	CD94 MACMU
3	178.5	17.3	179	1	NK11 MOUSE
4	178.5	17.3	179	1	CD94 HUMAN
5	173.5	16.9	199	1	CD94 PANTR
6	168	16.3	199	1	CD69 HUMAN
7	162.5	15.8	233	1	CD69 MOUSE
8	158.5	15.4	231	1	NKGC PANTR
9	158	15.4	233	1	NKGA PANTR
10	152.5	14.8	146	1	IXB TRIFL
11	151	14.7	233	1	NKGA HUMAN
12	150.5	14.6	148	1	CVXB CRODU
13	149	14.5	223	1	NK12 MOUSE
14	148	14.4	216	1	NKGD MACMU
15	147.5	14.3	359	1	CD72 HUMAN
16	146.5	14.2	163	1	V239 FOWPV
17	146.5	14.2	223	1	NK13 RAT
18	146	14.2	220	1	NK14 MOUSE
19	145	14.1	146	1	MMHB AGKHA
20	144	14.0	149	1	CLE2 HUMAN
21	144	14.0	216	1	NKGD HUMAN
22	144	14.0	240	1	NKGE HUMAN
23	144	14.0	301	1	LECI MOUSE
24	139.5	13.6	231	1	NKGC MACMU
25	139	13.5	157	1	MMHA AGKHA
26	139	13.5	304	1	MMGL MOUSE
27	138	13.4	167	1	V008 FOWPV
28	138	13.4	240	1	NKGE PANTR
29	138	13.4	301	1	LECI RAT
30	137.5	13.4	233	1	NKGA MACMU
31	137.5	13.4	1722	1	LY75 HUMAN
32	133	12.9	311	1	LECI HUMAN
33	132	12.8	548	1	KUCR MOUSE

RESULT 1

ID	CD94_MACMU	STANDARD;	PRT;	179 AA.
AC	Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Natural killer cells antigen CD94 (NK cell receptor) (Killer cell			
DE	lectin-like receptor subfamily D, member 1).			
GN	KURDI OR CD94.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=20322487; PubMed=10866118;			
RA	LaBonte M.L., Levy D.B., Letvin N.L.;			
RT	"Characterization of rhesus monkey CD94/NKG2 family members and			
RT	identification of novel transmembrane-deleted forms of NKG2-A, B, C,			
RT	and D.";			
RL	Immunogenetics 51:496-499 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=21158386; PubMed=11261935;			
RA	Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;			
RT	"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative			
RT	splicing of 5' exons in rhesus monkey decidua.";			
RL	Immunogenetics 53:69-73 (2001).			
CC	-1- FUNCTION: Plays a role as a receptor for the recognition of MHC			
CC	class I HLA-E molecules by NK cells and some cytotoxic T-cells.			
CC	-1- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family			
CC	members.			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=1; Synonyms=CD94-A;			
CC	Isoid=Q9MZK9-1; Sequence=Displayed;			
CC	Name=2; Synonyms=CD94-B;			
CC	Isoid=Q9MZK9-2; Sequence=VSP_003055;			
CC	Name=3; Synonyms=CD94 alt;			
CC	Isoid=Q9MZK9-3; Sequence=VSP_003054;			
CC	-1- TISSUE SPECIFICITY: Natural killer cells.			
CC	-1- SIMILARITY: Contains 1 C-type lectin family domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; AF190931; AAF74527.1; -.			
DR	EMBL; AF190932; AAF74528.1; -.			

ALIGNMENTS

P10716 rattus norv
P07306 homo sapien
P02707 gallus gall
P34927 mus musculu
P02706 rattus norv
P81397 agkistrodon
P81509 croatalus ho
P8114 trimeresu
P07897 rattus norv
P49259 bos taurus
P49260 oryctolagus
Q61282 mus musculu

34 128 12.4 550 1 KUCR RAT
35 127.5 12.4 290 1 LECH HUMAN
36 127 12.3 207 1 LECH CHICK
37 126 12.2 283 1 LECH MOUSE
38 126 12.2 283 1 LECH RAT
39 125.5 12.2 133 1 RHCA AGKRH
40 124.5 12.1 117 1 CHBB CROHO
41 124.5 12.1 123 1 ABAA TRIAB
42 123 12.0 2134 1 PGCA RAT
43 122.5 11.9 1463 1 PA2R BOVIN
44 122 11.9 1458 1 PA2R RABIT
45 122 11.9 2132 1 PGCA_MOUSE

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DR EMBL; AF190933; AAF74529.1; -.
DR EMBL; AF294886; AAG34498.1; -.
DR HSP; P22897; IREGG.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; LECTIN_C.1.
DR PROSITE; PS00615; C-TYPE LECTIN_2; 1.
DR Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 1 34 MAVPKTTLWRLISGTLGIICLSLMTGLILKNS -> MAA
(in isoform 3).
FT /FTID=VSP_003054.
FT L -> LQ (in isoform 2).
FT /FTID=VSP_003055.
FT Y -> D.
FT VARIANT 139 139
FT SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
Query Match 17.5%; Score 180.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 6e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRILCCGS-----KDSCTSHCPSPILLWTRNGS 84
DB 14 GTLGIIICSLMATIGILKLSVETPKLVSPEATPGNIELQKSDC--C-SCHKRWGVRC 70
QY 85 HCYFSEMEKQDWNLSKFCADKGSLLTFFPNQGVKLFGEYLQDFYIGLRNID---GW 141
DB 71 NCYFTSSSEKTNWNSRHFCASQSSLLQLQNRDELDFNSS--SQHFYIGLSYSEHTAW 128
QY 142 RWEQGPALSLILNLSLI---QRCGAIHRNG-LQASSCEVALQWICKVLY 187
DB 129 LWENGSAISQYLFFSPFTFKPKNCIAYNSKGNALDESCETKRNRYICKQOL 178

```

RESULT 2

```

NKIL MOUSE
ID NKIL_MOUSE STANDARD; PRT; 227 AA.
AC P27811;
DT 01-AUG-1992 (Rel. 23; Created)
DT 01-AUG-1992 (Rel. 23; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Natural killer cell surface protein Fl-2 (NKR-P1 2) (NKR-P1.7).
GN KIRBIA OR LY55A OR LY55.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giorda R., Trucco M.,
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013158; PubMed=1680927;
RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
RA Seaman W.E.;
RT "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
RT Identification of a natural killer cell gene complex on mouse
RT chromosome 6.";

```

```

J. Immunol. 147:3229-3236(1991).
-!- FUNCTION: May function as signal-transmitting receptor.
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Natural killer cells.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
CC EMBL; M77676; AAA39822.1; -.
CC EMBL; M77753; AAA39366.1; -.
CC PIR; A46467; A46467.
CC HSP; P22897; IREGG.
CC MGD; MGI:107540; K1rb1a.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_2; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_1; FALSE_NEG.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
FT DISULFID 94 105 BY SIMILARITY.
FT DISULFID 122 210 BY SIMILARITY.
FT DISULFID 189 202 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 39 S -> L (IN REF. 2).
FT SEQUENCE 227 AA; 25689 MW; 0599A2587DF0B615 CRC64;
Query Match 17.5%; Score 180.5; DB 1; Length 227;
Best Local Similarity 26.7%; Pred. No. 7.8e-11;
Matches 58; Conservative 33; Mismatches 95; Indels 31; Gaps 8;
QY 1 MADSIYSTLELPEAPQVQDESRLK---KAVLHRPHLSRFAMVALGLL---TVILMSL 53
DB 1 MDTARVYFGLKPPRTPGAWHESPSPDPACRPSRHSALKLSCAGLILLVVTIGMSV 60
QY 54 LMVQRIIC-----CG-----SKDSTCHSPCPTLWTRNGSHCYFVSEKKNWSS 99
DB 61 LV--RVLLQKFSIEKCYVLIQENLNKNTDCAKLECPQDWLSHRDKCFHVQSVNTWEEG 118
QY 100 LKFCADKGSLLTFFPNQGVKLFGEYLQDF--YWIGLRNI---DGNWEGGPALS---L 151
DB 119 LVDGCDGKATLMLIQDQELRFLDLSIKEKYNSEWIGLYRTPIDPMNWKWINGSTLNSDVL 178
QY 152 RILNLSIQRCGAIHRNGLOASSCEVALQWICKVLY 188
DB 179 KITGDTENDSCAAISGDKVTFESCNSDNRWICQKELY 215

```

RESULT 3

```

CD94_HUMAN
ID CD94_HUMAN STANDARD; PRT; 179 AA.
AC Q13241; O43321; O43773; Q9UBE3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 15-MAR-2004 (Rel. 43; Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
DE lectin-like receptor subfamily D, member 1) (KF43).
GN KIR2D1 OR CD94.

```



```

OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=96011848; PubMed=7589107;
RX Chang C., Rodriguez A., Carrtero M., Lopez-Botet M., Phillips J.H.,
RA Janier L.L.;
RT "Molecular characterization of human CD94: a type II membrane
RT glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carrtero M., Glienne J., Beillon T., Ramirez A.,
RA Lehrach H., Francis F., Lopez-Botet M.;
RT "Structure of the human CD94 C-type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Biassoni R.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RL Immunogenetics 48:87-88(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q13241-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q13241-2; Sequence=VSP_003053;
CC Name=3; Synonyms=CD94 alt;
CC IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD94 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".

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CC -----
DR EMBL; U30610; AAC50291.1; -
DR EMBL; Y14287; CAA74663.1; -
DR EMBL; Y14288; CAA74663.1; JOINED.
DR EMBL; AJ000673; CAA04230.1; -
DR EMBL; AJ000001; CAA03845.1; -
DR EMBL; AB009597; BAA24450.1; -
DR EMBL; AB010084; BAA24451.1; -
DR EMBL; BC028009; AAH28009.1; -
DR DBJ; 1B6E; 15-JUN-99.
DR Genew; HGNC:6378; KLRD1.
DR MIM; 602894; -
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004888; P:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . ; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SMC0034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34 MAVEKTLMLRLISGLTGLICLSLMTATLIGLLKNS -> MAA
FT FT (in isoform 3)
FT FT /FTID=VSP_003052.
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT FT /FTID=VSP_003053.
SQ SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLITVILMSLLMYQRIILCCG-----KDTCTGCHPCPCILWTRNGS 84
DB 14 GTLIGILCLSLMATLIGLLKNSFTKLSTEPAPTPGPNIELQKSDC--C-SCQEKWVYRC 70
QY 85 HCYYFNEKKDWNSLKFCAKDGSHLLTTPDNGVKLFGYLGQDFYGLRNLID--GW 141
DB 71 NCYFISSEKQTWNEHRHLCAKSSQLLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPAISRLITN---SLIQCGAIHRNG-LQASCEVALQWICKVVL 187
DB 129 LWENGSAISQYLPFPSTFTPTNKNCIAYPNGNALDESCDKNYICKQQL 178
RESULT 4
CD94_PANTR
ID CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9WZ41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell

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DE DE lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20350666; PubMed=10894168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Vallante N.M., Lanier L.L.,
RA Parham P.;
RT "Rapid evolution of NK cell receptor systems demonstrated by
RT comparison of chimpanzees and humans.";
RL Immunity 12:687-698(2000).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=21623889; PubMed=11751968;
RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
RT NK32 genes.";
RL J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MZ41-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MZ41-2; Sequence=VSP 003056;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
DR EMBL; AF259054; AAF86964.1; -.
DR HSSP; P22897; IEGG.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 105 105 L -> LQ (in isoform 2).
FT /FTID=VSP 003056.
SQ SEQUENCE 179 AA; 20493 MW; 7244D99E8D9587E7 CRC64;

Query Match
Best Local Similarity 17.3%; Score 178.5; DB 1; Length 179;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

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QY 44 GLLTIVLMSLLMYQRIILCCGS-----KSTSCHPSCPILWTRNGS 84
DB 14 GTLGIIICLSMATLIGLLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SQEKWVGXRC 70
QY 85 HCYYFSMEKDDWNSSSLKFCADKGSLLTTPPNQGVKLFGEYLGQDFYWGIRNID---GW 141
DB 71 NCYFTISSEKQTNESRHLCAQSKQSLQLQNTDELDFMSS--SQQFYWIGLSSEHTAW 128
QY 142 RWEGSGPALSILRLTNSLI---ORCGATHRNG-LQASSCEVALQMTCKKVL 187
DB 129 LWENGSAISQYLFFSFETFPNFCIAYNPNGNALDESCEDKNRYICKQOL 178

RESULT 5
CD69_HUMAN STANDARD; PRT; 199 AA.
ID CD69_HUMAN
AC Q07108;
DC 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Early activation antigen CD69 (Early T-cell activation antigen p60)
DE (GP32/28) (Leu-23) (MLR-3) (EAL) (BL-AC/P26) (Activation inducer
DE molecule) (AIM).
GN CD69.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93267093; PubMed=8496594;
RA Hamann J., Fiebig H., Strauss M.;
RT "Expression cloning of the early activation antigen CD69, a type II
RT integral membrane protein with a C-type lectin domain.";
RL J. Immunol. 150:4920-4927(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 96-103; 128-146 AND 189-199.
RC TISSUE=Blood;
RX MEDLINE=93340630; PubMed=8340758;
RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
RA Esch F., Sanchez-Mateos P., Sanchez-Madrid F.;
RT "Molecular cloning, expression, and chromosomal localization of the
RT human earliest lymphocyte activation antigen AIM/CD69, a new member
RT of the C-type animal lectin superfamily of signal-transmitting
RT receptors.";
RL J. Exp. Med. 178:537-547(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314711; PubMed=8100776;
RA Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
RA Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
RA Alderson M.R.;
RT "Molecular characterization of the early activation antigen CD69: a
RT type II membrane glycoprotein related to a family of natural killer
RT cell activation antigens.";
RL Eur. J. Immunol. 23:1643-1648(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94298875; PubMed=8026529;
RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.;
RT "Structure of the gene coding for the human early lymphocyte
RT activation antigen CD69: a C-type lectin receptor evolutionarily
RT related with the gene families of natural killer cell-specific
RT receptors.";
RL Eur. J. Immunol. 24:1692-1697(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZE1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS0041; C TYPE LECTIN 2; 1.
DR Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
KW Phosphorylation.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 62 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 195 C-TYPE LECTIN.
FT DISULFID 68 85 BY SIMILARITY.
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 199 AA; 22517 MW; 39F8E4941D36D4F6 CRC64;

Query Match 16.3%; Score 168; DB 1; Length 199;
Best Local Similarity 24.1%; Pred. No. 1.2e-09;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 5;

QY 38 FAWALGLLTIVILMSLL-----MYQRIILCCGSKDSTCSHCPCPILWTRNGSHC 86
Dy 43 WAVILVILITSLIALALNKGKYNCPGLYEKL-----ESSDHHVATCKNEWSYKRTC 96
QY 87 YFYSMEKKDMNSSLKFCADKSGHLLTFPDNGVGLFGYLGQDFYWGILRN--IDGWRWE 144
Dy 97 YFSTTYKSWALQSCSDAATLAVIDSEKDMTFLKRYSELEHWGLKNEAQTWKWA 156

QY 145 GGPAL-SRLITNSLIQRCGAHNRNGLOASCEVALQWICKK 185
Dy 157 NGKEFNWFNLTGSG--GRCSVNHNKVTAVDCEANFHWVCSK 196

RESULT 7
NKGC PANTR STANDARD; PRT; 233 AA.
AC Q9QME8; Q9MZ38; Q9MZ40;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE NKGC-2004 (Rel. 43, Last annotation update)
DE NKGC-C type II integral membrane protein (NKGC-C activating NK
DE receptor) (NK cell receptor C).
GN KLRC2 OR NKGC2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-60 AND 232-TYR-ARG-233 DEL.
RX MEDLINE=20350666; PubMed=10894168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Valiente N.M., Lanier L.L.,
RA Farham P.;
RT "Rapid evolution of NK cell receptor systems demonstrated by
RT comparison of chimpanzees and humans.";
RL Immunity 12:687-698(2000).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
CC Class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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DR EMBL; AF259057; AAF86967.1; -.
DR EMBL; AF259059; AAF86969.1; -.
DR EMBL; AF259060; AAF86970.2; -.
DR HSP; P05451; LLIT.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS0041; C TYPE LECTIN 2; 1.
DR Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 229 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 145 227 BY SIMILARITY.
FT DISULFID 206 219 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 60 60 N -> D (in allele NKG2-C*101).
FT VARIANT 232 233 Missing (in allele NKG2-C*103).
SQ SEQUENCE 233 AA; 26169 MW; 18C04D1B91E1B7CA CRC64;

Query Match 15.8%; Score 162.5; DB 1; Length 233;
Best Local Similarity 25.4%; Pred. No. 5.1e-09;
Matches 43; Conservative 28; Mismatches 83; Indels 15; Gaps 5;

QY 33 PHLRFAMVALGLLTIVILMSLLMYQRIILCCGSKDSTCS-----HCPCPILWTRNG 83
Dy 66 PPPEKLFAVLGIICVIMATVLTIVILPELQNNSSPNTGTOKARHCHGCPWEIYIS 125
QY 84 SHCYFYSMEKKDMNSSLKFCADKSGHLLTFPDNGVGLFGYLGQDFYWGIL-RNIDGWR 142
Dy 126 NSCYIYICKERTWEESLLACTSKNSGLLSIDNEEMKFLATISPS--WIGVFNSSHP 183

QY 143 WE--GGPALSLRLITNSLIQ--RCGAHNRNGLOASCEVALQWICKKVLVY 188
Dy 184 WVTINGLAFLKHEIIDSDAELNCAVLQVGLKLSAQCGSSIIYHCKHKLY 232

RESULT 8
NKGC HUMAN STANDARD; PRT; 231 AA.
AC P26717; O43802; Q9NR42;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NKGC-C type II integral membrane protein (NKGC-C activating NK
DE receptor) (NK cell receptor C).
GN KLRC2 OR NKGC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKGC2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RN J. Exp. Med. 173:1017-1020(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Glienke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Lehrach H., Hofer E., Francis F.;
RT "The genomic organization of NKGC2C, E, F, and D receptor genes in the

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47 TWADAEKFTQOHTGSHLVSPHSTEEVDVVVQTHQSLKSTFFWIGANNIWNKCNQWQSD 106

Db 172 ASSCEVALQWICKKVL 187
QY 146 G 146
Db 107 G 107

RESULT 13

NK12 MOUSE

ID NK12 MOUSE STANDARD; PRT; 223 AA.

AC P27812;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Convulxin beta precursor (CVX beta).

OS Crotalus durissus terrificus (South American rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OC NCBI_TaxID=8732;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=91349596; PubMed=1880421;

EX MEDLINE=91349596; PubMed=1880421;

RA "Mouse NK1-P1. A family of genes selectively coexpressed in adherent

RT lymphokine-activated killer cells.";

RT Biochem. J. 333:389-393(1998).

RL J. Immunol. 147:1701-1708(1991).

RN [2]

RP SEQUENCE OF 1-29 FROM N.A.

RP MEDLINE=9238663; PubMed=1517565;

RA Giordano R., Weisberg E.P., Ip T.K., Trucco M.;

RT "Genomic structure and strain-specific expression of the natural

RT killer cell receptor NK1-P1.";

RL J. Immunol. 149:1957-1963(1992).

RN [1]

CC -!- FUNCTION: May function as signal-transmitting receptor.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- TISSUE SPECIFICITY: Natural killer cells.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; M77677; AAA39823.1; -

DR EMBL; X64721; CAA45974.1; -

DR PIR; B46467; B46467.

DR MGI; MGI:107539; Klrblb.

DR InterPro; IPR002353; Antifreeze21.

DR InterPro; IPR001304; Lectin C.

DR Pfam; PF00059; lectin_c_1.

DR PRINTS; PR00356; ANTIFREEZE21.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.

DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.

KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.

FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT

FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).

FT DISULFID 94 105 BY SIMILARITY.

FT DISULFID 122 210 BY SIMILARITY.

FT DISULFID 189 202 BY SIMILARITY.

FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 223 AA; 25157 MW; 8D04C11DEB9C56 CRC64;

SQ

Query Match 14.5%; Score 149; DB 1; Length 223;

QY 172 ASSCEVALQWICKKVL 187

Db 218 SAQCSSIIYCHKHL 233

RESULT 12

CVXB CRODU

ID CVXB CRODU STANDARD; PRT; 148 AA.

AC O93427;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Convulxin beta precursor (CVX beta).

OS Crotalus durissus terrificus (South American rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OC NCBI_TaxID=8732;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=98324901; PubMed=9657980;

EX MEDLINE=98324901; PubMed=9657980;

RA Leduc M., Bon C.;

RT "Cloning of subunits of convulxin, a collagen-like platelet-

RT aggregating protein from Crotalus durissus terrificus venom.";

RL Biochem. J. 333:389-393(1998).

RN [1]

CC -!- FUNCTION: Binds to the platelet and collagen receptor,

CC glycoprotein VI (GPVI).

CC -!- SUBUNIT: Heterohexamer of three alpha chains and three beta

CC chains; disulfide-linked.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC

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CC

DR EMBL; Y16349; CAA76182.1; -

DR HSP; P23807; I1XX.

DR InterPro; IPR001304; Lectin C.

DR InterPro; IPR003990; Pancreatis_ac.

DR Pfam; PF00059; lectin_c_1.

DR PRINTS; PR01504; PNCREATITSP.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.

DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.

KW Lectin; Glycoprotein; Signal.

FT SIGNAL 1 23 CONVULXIN BETA.

FT CHAIN 24 148 C-TYPE LECTIN.

FT DOMAIN 34 145 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)

FT DISULFID 26 26 (POTENTIAL).

FT BY SIMILARITY.

FT BY SIMILARITY.

FT INTERCHAIN (WITH C-104 IN ALPHA CHAIN)

FT (POTENTIAL).

FT BY SIMILARITY.

FT SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

SQ

Query Match 14.6%; Score 150.5; DB 1; Length 148;

Best Local Similarity 31.4%; Pred. No. 4.9e-08;

Matches 38; Conservative 18; Mismatches 42; Indels 23; Gaps 6;

QY 35 LSRFAMVAGLTLVILMLYQRLCCGSKDSTCHSPILWTRNGSHCYFYSMEKK 94

Db 1 MGRFIFVSPGLL-VVPSL-----SGSEAGFC-----CPSHWSYDRYCYKVKQEM 46

QY 95 DNNSSILKFCADK-GSHLTFDPNQ-----VKLFGYLQDFFWIGLRLNI---DGRWREG 145

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:11:32 ; Search time 32.6089 Seconds

(without alignments)
1819.059 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSLLELPEAPQVD.....GLQASCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	188	11	O88713
2	838	81.4	188	11	O64335
3	568.5	55.2	189	4	O75613
4	564.5	54.9	195	4	O96E93
5	548.5	53.3	189	4	O43198
6	182	17.7	257	13	Q90636
7	180.5	17.5	227	11	Q91V25
8	180	17.5	179	11	O54708
9	180	17.5	179	11	O54707
10	179.5	17.4	227	11	O925G4
11	179.5	17.4	227	11	Q61973
12	177.5	17.2	179	6	Q8MH78
13	177	17.2	233	6	Q8MJH7
14	177	17.2	236	6	Q95L94
15	177	17.2	275	11	Q9D403
16	176	17.1	233	6	Q8MJH6

17	175	17.0	233	6	Q8MJ10	Q8mj10 pongo pygma
18	174.5	17.0	179	6	Q8MJ13	Q8mj13 pongo pygma
19	174.5	17.0	179	6	Q8MH19	Q8mh19 pongo pygma
20	174.5	17.0	200	6	Q8SPX1	Q8spx1 sus scrofa
21	174.5	17.0	231	6	Q9MZK3	Q9mzk3 macaca mula
22	173	16.8	231	6	Q8MI05	Q8mi05 macaca fasc
23	172	16.7	233	6	Q8MJH8	Q8mjh8 pongo pygma
24	171.5	16.7	179	6	Q8MJ14	Q8mj14 pongo pygma
25	171.5	16.7	181	4	Q9NZS1	Q9nzs1 homo sapien
26	170.5	16.6	231	6	Q9GK88	Q9gk88 macaca mula
27	169.5	16.5	200	13	Q802S8	Q802s8 gallus gall
28	169	16.4	159	6	Q8SPX0	Q8spx0 sus scrofa
29	168	16.3	165	11	Q9P007	Q9p007 mus musculus
30	168	16.3	233	6	Q8MJH5	Q8mjh5 pongo pygma
31	168	16.3	233	6	Q8MJH9	Q8mjh9 pongo pygma
32	167	16.2	233	6	Q8MJ11	Q8mj11 pongo pygma
33	167	16.2	246	6	Q9MZK2	Q9mzk2 macaca mula
34	166.5	16.2	231	4	Q9NZS2	Q9nzs2 homo sapien
35	165	16.0	246	6	Q9MZK1	Q9mzk1 macaca mula
36	164.5	16.0	225	4	Q12918	Q12918 homo sapien
37	163.5	15.9	146	13	Q9IAM0	Q9iam0 agkistrodon
38	163.5	15.9	146	13	Q8JIW1	Q8jiw1 agkistrodon
39	163.5	15.9	191	4	Q9UHP7	Q9uhp7 homo sapien
40	163	15.8	161	6	Q95JG4	Q95jg4 bos taurus
41	162.5	15.8	233	6	Q9GME8	Q9gme8 pan troglod
42	162.5	15.8	233	6	Q9MZ40	Q9mz40 pan troglod
43	161.5	15.7	223	11	Q925G3	Q925g3 mus musculus
44	161.5	15.7	226	6	Q9MZ39	Q9mz39 pan troglod
45	161.5	15.7	334	4	Q96QP9	Q96qp9 homo sapien

ALIGNMENTS

RESULT 1

O88713 ID O88713 PRELIMINARY; PRT; 188 AA.
AC O88713;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
DE like receptor G1).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raulet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACFB; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue of MAFA.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AAK40082.1; -.
DR MGD; MGI:1355294; Klrp1.

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DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0005529; F: sugar binding; IEA.
DR GO: 0007157; P: heterophilic cell adhesion; IEA.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match      100.0%; Score 1029; DB 11; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
Db 1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL 60

Qy 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMEKKDWNSSLKFCADKSGSHLLTFPDNQGVK 120
Db 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMEKKDWNSSLKFCADKSGSHLLTFPDNQGVK 120

Qy 121 LFGEYLGQDFYWGILRNIDGWRWEGGPPALSIRILTNLSLIQRCGAHNRNGLOASCEVALQ 180
Db 121 LFGEYLGQDFYWGILRNIDGWRWEGGPPALSIRILTNLSLIQRCGAHNRNGLOASCEVALQ 180

Qy 181 WICKKVL 187
Db 181 WICKKVL 187

RESULT 3
075613 PRELIMINARY; PRT; 189 AA.
ID 075613;
AC 075613;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ITIM-containing receptor MAFA-L.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat '51', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL: AF081675; AAC32200.1; -
DR EMBL: AF097358; AAO30719.1; -
DR GO: GO:0005529; F: sugar binding; IEA.
DR InterPro: IPR001304; Lectin C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
DR SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match      55.2%; Score 568.5; DB 4; Length 189;
Best Local Similarity 57.2%; Pred. No. 2.3e-51;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

Qy 1 MADSSIYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
Db 1 MTDSVIYSLMLPTATQANDYGPQKSSSRPSCSCICLVAIALGLLTAVALLSVLLYQWIL 60

Qy 61 CCGSKDSTCSHCPCPIILWTRNGSHCYFFSMEKKDWNSSLKFCADKSGSHLLTFPDNQGVK 120
Db 61 CCGSNYSTCASCPCPDPRWVKYGNCHYFFSVEEKDWNSSLKFCARSHLLVITDQMS 120

Qy 121 LFGEYLGQDFYWGILRNIDGWRWEGGPPALSIRILTNLSLIQRCGAHNRNGLOASCEVAL 179
Db 121 LLQVLFSEAFQWIGLRNNSGWRWEDGPPALSIRILTNLSLIQRCGAHNRNGLOASCEVAL 180

Qy 180 QWICKV 186
Db 181 HWCKKV 187

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RESULT 4
Q96E93 PRELIMINARY; PRT; 195 AA.
AC Q96E93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to killer cell lectin-like receptor subfamily G, member
DE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012621; AAH12621.1; -.
DR GenBank; HGNC:6380; KIRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 195 AA; 21831 MW; 178EE98E08BEC473 CRC64;

Query Match 54.9%; Score 564.5; DB 4; Length 195;
Best Local Similarity 57.08; Pred. No. 6.1e-51;
Matches 106; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRLPHLSRFAMVALGLLTIVILMSLIMYQRI 60
DB 1 MTDVSIYSMLELPTATQAQNDYGPQKSSSRSCSLVAIALGLITAVLLSVLLQWIL 60
QY 61 CGSKSTCHSCPCPILWTRNGSHCYFYSMEKKNSSLKFCADKSGHLLTFFPDNGVK 120
DB 61 CGSNYSTCASCPCPDRWKYGNHCYFVSVEKDNSSLEFCLARDSHLLVITDQEMS 120
QY 121 LFGEYLQDGYFWIGLRNIDGWRWEGGPAISL-RILTNSLIQRCGAIHNGLQASSCEVAL 179
DB 121 LLQVFLSEAFWIGLRNNSGWRWEDGSLNFSRISSNFVQTCGAINKNGLQASSCEVPL 180
QY 180 QWICKK 185
DB 181 HWCKK 186

Query Match 54.9%; Score 564.5; DB 4; Length 195;
Best Local Similarity 57.08; Pred. No. 6.1e-51;
Matches 106; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRLPHLSRFAMVALGLLTIVILMSLIMYQRI 60
DB 1 MTDVSIYSMLELPTATQAQNDYGPQKSSSRSCSLVAIALGLITAVLLSVLLQWIL 60
QY 61 CGSKSTCHSCPCPILWTRNGSHCYFYSMEKKNSSLKFCADKSGHLLTFFPDNGVK 120
DB 61 CGSNYSTCASCPCPDRWKYGNHCYFVSVEKDNSSLEFCLARDSHLLVITDQEMS 120
QY 121 LFGEYLQDGYFWIGLRNIDGWRWEGGPAISL-RILTNSLIQRCGAIHNGLQASSCEVAL 179
DB 121 LLQVFLSEAFWIGLRNNSGWRWEDGSLNFSRISSNFVQTCGAINKNGLQASSCEVPL 180
QY 180 QWICKK 185
DB 181 HWCKK 186

RESULT 5
O43198 PRELIMINARY; PRT; 189 AA.
AC O43198;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=96438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAF has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212 (1998).
DR EMBL; AF034952; AAC34731.1; -.

Query Match 17.7%; Score 182; DB 13; Length 257;
Best Local Similarity 28.7%; Pred. No. 8.6e-11;
Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;

QY 32 RPHLSRFAMVALG---LLTVILMSLIMYQRI--CGSKSTCHSCPCPILWTRNGSHCY 87
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Db 86 QNRRRLCVLSPVPCMLVAVIVLQRPSC--SPRPFSHV--CPNAVWFGQKCY 141
QY 88 YFSMEKKDWNSSLKFCADKAGSHLLTFPDNQGVKLFGEYLGQDFYWGILRNDG---WEWE 144
Db 142 YFSTESDWNSSRHHCHRLGASLALDTKEMEFLQYQRPADRWIGLHRAEGDEHWTWA 201
QY 145 GGPALSLRLNLSLI-----QRCIAHRNGLOASSCEVALQWICKK 185
Db 202 DQSA-----FTNRPFELRGGRGCRAYLNGDGISSALCHSEKFEWVCSR 243

RESULT 7
Q91V25 PRELIMINARY; PRT; 227 AA.
AC Q91V25;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NKR-PIA (Natural killer cell receptor protein NKR-PIA).
GN KLRB1A OR NKR-PIA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Plougastel B.F.M., Yokoyama W.M.;
RT "Mouse NKR-PIA gene, genomic structure.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
EX MEDLINE=99248165; PubMed=10229823;
RA Kung S.K., Su R.C., Shannon J., Miller R.G.;
RT "The NKR-P1b gene product is an inhibitory receptor on SJL/J NK
cells.";
RL J. Immunol. 162:5876-5887(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kung S.K.P., Su R.C., Shannon J., Miller R.G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF285840; AAK83003.1; -.
DR EMBL; AF285839; AAK83003.1; JOINED.
DR EMBL; AF354262; AAK39102.1; -.
DR MGD; MGI:107540; Klrbl1a.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 227 AA; 25715 MW; CCB8324AE07FBB97 CRC64;

Query Match 17.5%; Score 180.5; DB 11; Length 227;
Best Local Similarity 26.5%; Pred. No. 1.1e-10;
Matches 57; Conservative 32; Mismatches 99; Indels 27; Gaps 7;

QY 1 MADSIYSTLELPEAPQVQDSRWKLKAVLHR-PHLGRFAM-----VALGLLTIVILMSLLM 55
Db 1 MDTARVYGLKPRPTPGAWHSPSPSPDACPSPSRHLALKLSCAGLILVLTIGMSV 60
QY 56 YQRIILC-----CG-----SKDSTCSHCPSCEILWTRNGSHCYFSEKKDWNSSLK 101
Db 61 LVRVLIOKPSIEKCVLILQENLNKTTDCSAKLECPQDWLSHRDKCFHVSQVSNTWEEGLV 120
QY 102 FCADKGSLLTFFPDNQGVKLFGEYLGQDF--YNTGLRNI-----DCWRWEGGPAIS--LRI 153
Db 121 DCDGKATMLIQDQEEELRFLDSIKEKYNFWLGLRYTLTLPDMNWKWINGSTLNSDLVKI 180
QY 154 LTNSLIQRCGAIHRNGLOASSCEVALQWICKVLY 188

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Db 181 TGDITENDSCRAISGKVTFFESCNSDNRWICQKELY 215

RESULT 8
Q54708 PRELIMINARY; PRT; 179 AA.
AC Q54708;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD94.
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB.17 SCID;
EX MEDLINE=98124458; PubMed=9464811;
RA Vance R.E., Tanamachi D.M., Hanke T., Raulat D.H.;
RT "Cloning of a mouse homolog of CD94 extends the family of C-type
lectins on murine natural killer cells.";
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrcl.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59E1CBB63139E45 CRC64;

Query Match 17.5%; Score 180; DB 11; Length 179;
Best Local Similarity 31.8%; Pred. No. 9.2e-11;
Matches 57; Conservative 25; Mismatches 75; Indels 22; Gaps 9;

QY 22 SRWKLKAVLHRPHLSRFAMVALGLLTIVILMSLMYQRIILCGSKDST-----CSHCPSCP 76
Db 7 TRWELMSVIFGIK-CLEFLMTVLG---VLLINSFTIQITQSPSTTTVEFQEVSECCVCL 62
QY 77 ILWTRNGSHCYFSEMEKKDWNSSLKFCADKAGSHLLTFPDNQGVKLFGEYLGQDFYWGIL- 135
Db 63 DKWVGHQCNCFYTSKEEKSWERSRDFCASONSSLQ--PQSRNELSFMNF-SQTFFWIGMH 120
QY 136 ----RNIDGWRWEGGPALSLRLTN-SLIQRCGAI---HRNGLOASSCEVALQWICKKV 186
Db 121 YSEKRN-AWLWEDGTVPKDLFFEFVIRPEHCIVYSPSKSVSAESCENKRYICKKL 177

RESULT 9
Q54707 PRELIMINARY; PRT; 179 AA.
AC Q54707;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE DE Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Vance R.E., Tanamachi D.M., Hanke T., Raulat D.H.;
RL Eur. J. Immunol. 27:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.

```



```
QY 54 LMVORILC-----CG-----SKDSTCSHCPCPILWTRNGSHCYFYSMEKKDWNS 99
DB 61 LV--RVILQKSEIKCYVILQENLNKTTDCSAKLECPQDWLSHRDKCFHSHVSNWTWEEG 118
QY 100 LKFCADKGGSHLLTFPDNGVKLFGEYLQDF--YWIGLRNI---DGMWEGGPALS---L 151
DB 119 LVDGCGKATMLIQDQELRFLDSIKEKYNFWIGLRVYTLPDNWKWINGSTLNSDVL 178
QY 152 RILNLSLQRCAGHRNGLQASSCEVALQWICKVLY 188
DB 179 KITDDTENDSCAALSGDKVTFPSCNSDNRWICQKELY 215

RESULT 12
Q8MHY8 PRELIMINARY; PRT; 179 AA.
AC Q8MHY8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Natural killer cell receptor.
GN POPY-CD94.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_taxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470381; AAM78481.1; -.
DR EMBL; AF470382; AAM78482.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
KW Receptor.
SQ SEQUENCE 179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;

Query Match 17.2%; Score 177.5; DB 6; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.7e-10;
Matches 54; Conservative 16; Mismatches 69; Indels 31; Gaps 7;

QY 44 GLLTVILSLMYQRIICGS-----KSTCSHCPCPILWTRNGS 84
DB 14 GTLGILICLSMATGILKNSFTKLSIEPAFTPGPDIBLQKSDC--C-SQCKWVGYRC 70
QY 85 HCYFYSMEKKDWNSLKCADKGGSHLLTFPDNGVKLFGEYLQDFYWIGLRNI---GW 141
DB 71 NCYFISSEQKWTNRSRHLCAQKSSLLQIQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEQGPALS---LRILTNSLIQRCAGHRNG--LQASSCEVALQWICKVLY 187
DB 129 LWENGSAISQVLPFLPFTFNPKNCTAYVFNPGNALDESCECDKNRYICKQOL 178

RESULT 13
Q8MJH7 PRELIMINARY; PRT; 233 AA.
AC Q8MJH7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Natural killer cell lectin-like receptor.
```

```
GN POPY-NKG2A.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_taxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
RT Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470395; AAM78495.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Receptor; Lectin.
SQ SEQUENCE 233 AA; 26239 MW; 6B8AE8489BAD2686 CRC64;

Query Match 17.2%; Score 177; DB 6; Length 233;
Best Local Similarity 24.5%; Pred. No. 2.6e-10;
Matches 48; Conservative 28; Mismatches 84; Indels 36; Gaps 6;

QY 7 YSTLELPEAPQVQDESRLKXAVLHRPHLSFAMVALGLLTVILM-----SLLM 55
DB 59 YHKDLPSAPE-----KLIVGILGILCLVLMASVVTIWIPTLIQ 99
QY 56 YQRIILCGSKDSTCSHCPCPILWTRNGSHCYFYSMEKKDWNSLKCADKGGSHLLTFPD 115
DB 100 KHNSSSLNTRTQKAHRCGHCPPEWITVNSCYIYIGKERTWEESLLACASNSLLSDN 159
QY 116 NQGVKLFGEYLQDFYWIGL--RNIDGFWFE--GGPALSRLITLSLIQR--CGAIHRNGLIQ 171
DB 160 EEMKFLGTILPSS--WIGVFNSSHPVWVINGLAFQKEIKDSNADHDCAVLHTRGLR 217
QY 172 ASSCEVALQWICKVLY 187
DB 218 SNKCGSSILYHCKHKL 233

RESULT 14
Q95L94 PRELIMINARY; PRT; 236 AA.
AC Q95L94;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NK2-F3.
GN NK2-F3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_taxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Letvin N.L.;
RT "Analysis of rhesus monkey CD94/NKG2 family members.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395617; AAK97464.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 236 AA; 26365 MW; 1967FAEF3641351E CRC64;
```


Query Match 17.2%; Score 177; DB 6; Length 236;
Best Local Similarity 25.0%; Pred. No. 2.6e-10;
Matches 47; Conservative 33; Mismatches 82; Indels 26; Gaps 7;
QY 20 DESRWKLKAVLHRLPHLSRFAWALGLTLVILMSILMYQRIL--CCG-----S 64
DB 55 NDKTYHCKGLGPPPP--EKLTAELVIGIICIVIMATVLKTVVILPICIGLEQNFSNLRIQ 112
QY 65 KDSCTCHPCSPILWTRNGSHCHYFYSMEKQWNSSLKFCADKSHLLTFPDNQGKVLFG 124
DB 113 KAYDCGCHPEWITYTNS---CYIGKEKRTWEESLTCASKNSLLSIDNEEMQLLGS 169
QY 125 YLGQDFYWGILNRIDG--WRWEGGPALSLRIITNSL-IQRCGAIHRNGLOASSCEVALQ 180
DB 170 L--SVLSWVGVSRSDDHPWVSINGSTFKLIAESDICKENCVMHLSSGLKSHRCGASQL 227
QY 181 WICKKVLV 188
DB 228 YTCKKHLW 235

RESULT 15

Q9D403 PRELIMINARY; PRT; 275 AA.
AC Q9D403;
DT 01-JUN-2001 (T-REMBLrel. 17, Created)
DT 01-JUN-2001 (T-REMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-REMBLrel. 25, Last annotation update)
DE 4933425B16RIK protein.
GN 4933425B16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK016908; BAB30491.1; -.
DR HSSP; P23807; IIXX.
DR MGD; MGI:1918433; 4933425B16RIK.
DR GO; GO:0005529; F-sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;

Query Match 17.2%; Score 177; DB 11; Length 275;
Best Local Similarity 31.7%; Pred. No. 3.1e-10;
Matches 40; Conservative 17; Mismatches 57; Indels 12; Gaps 5;
QY 72 CPSCPILWTRNGSHCHYFYSN-EKKDWNSSLKFCADKSHLLTFPDNQGKVLFGYLGQ-- 128

mis Page Blank (uspto)

composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFA protein

Sequence 188 AA:
SQ

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CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 188 AA;

    Query Match      81.4%; Score 838; DB 2; Length 188;
    Best Local Similarity 80.7%; Pred. No. 3.2e-82;
    Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0

Qy 1 MADSSYSTLTLELPEAPOVDSESRWKLKAVLHRPHLSRFAMVALGLTTLVILMSLLMYQRL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MADNSYSTLTLELPAAPRVQDSDRRKVKAVLHRPCVSYLVAVLGLTTLVILMSLLYQRL 60

Qy 61 CCGSKDSTCTSCHPCSPILMTWNGSHCYFFSMEKDWNSSLKFCADKGGSHLLTFPDNQGVK 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 CCGSKGFMCSCSRCPNLWMNGSHCYFFSMEKRDWNSLKFADKGGSHLLTFPDNQGVN 120

Qy 121 LFGVYLGDGFYWIGLIDGWRWEGGPALSLRLTNSLIQRCGATHRNGLOASSCEVALQ 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 LFQYVGEDFYWIGLRIDGWRWEDGPALSLILSNSVYQCKGTHRCGLHASSCEVALQ 180

Qy 181 WICKKVL 187
   |||:|||||
Db 181 WICEKVL 187
   |||:|||||

RESULT 3
AAW88277
ID AAW88277 standard; protein; 188 AA.
XX AC AAW88277;
XX DT 29-MAR-1999 (first entry)
XX DE
XX KW Mast cell function-associated antigen (MAFA).
XX KW Mast cell function-associated antigen; MAFA; splice variant; rat;
XX KW Inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX OS Rattus sp.

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Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.

Claim 12; Page 37; 54pp; English.

A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in

XX The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 189 AA;

Query Match 55.2%; Score 568.5; DB 7; Length 189;
Best Local Similarity 57.2%; Pred. No. 4.8e-53;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;
QY 1 MADSIYSTLELPEAPQVQDSRWKIKAVLHRLPHLSRFAMVALGLLTVILMSLLMYQRIL 60
DB 1 MTDSVIYSMLPLTATQANDYGPQKSSSRPSCSLVAIALGLLTAVLLSVLLYQWIL 60
QY 61 CCGSKDSCSCHPCPIILWTRNGSHCYFYSMEKDWNSLKFCDKAGSHLLTFPDNQGVK 120
DB 61 CCGSNYSTCASCPCPDWRMKYGNHCYFYSVEEKDWNSLEFCLARDSHLLVITDQEMS 120
QY 121 LFGVYLQDFYWGILNRDGNRWEGGPAISL-RILTNSLIQRCGATHRNGLOASSCEVAL 179
DB 121 LLOVFLSAFCWIGLRNNSGNRWEDGSPINFSRISNSFVQTCGAINKNGLOASSCEVPL 180
QY 180 QWICKKV 186
DB 181 HWVCKKV 187

RESULT 6

AAR77472
ID AAR77472 standard; protein; 114 AA.

XX AAR77472;

XX 01-FEB-1996 (first entry)

XX

DE Partial sequence of mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
XX prevention.
OS Rattus rattus.
PN W09527734-A1.
PD 19-OCT-1995.
XX 06-APR-1995; 95WO-US004258.
XX 08-APR-1994; 94IL-00109257.
XX (YEDA) YEDA RES & DEV CO LTD.
PA (RYCU/) RYCUS A.
XX Pecht I, Guthmann MD, Tal M;
DR WPI; 1995-366356/47.
DR N-PSDB; AAT01471.
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX Disclosure; Page 38; 54pp; English.
XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX SQ Sequence 114 AA;
Query Match 53.5%; Score 551; DB 2; Length 114;
Best Local Similarity 84.1%; Pred. No. 1.9e-51;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 75 CPILWTRNGSHCYFYSMEKDWNSLKFCDKAGSHLLTFPDNQGVKLFGEYLQDFYWG 134
DB 1 CPILWTRNGSHCYFYSMEKDWNSLKFCDKAGSHLLTFPDNQGVNLFQYVGDFYWG 60
QY 135 LRNDGWRWEGGPAISL-RILTNSLIQRCGATHRNGLOASSCEVALQWICKKV 187
DB 61 LRNDGWRWEDGPAISLSNSVQKGTIHRGHLASSCEVALQWICKKV 113
RESULT 7
AAR89265
ID AAR89265 standard; protein; 189 AA.
XX AAR89265;
XX 29-MAR-1999 (first entry)
XX Human mast cell function-associated antigen (MAFA).
XX Mast cell function-associated antigen; MAFA; splice variant; human;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 7..10
FT /note= "ITIM motif"
FT Modified-site 65..67
FT /note= "Asn is N-glycosylated"
FT Modified-site 97..99
FT /note= "Asn is N-glycosylated"
FT Modified-site 137..139

FT /note= "Asn is N-glycosylated"
 PT 150..152
 FT /note= "Asn is N-glycosylated"
 XX
 PN WO9854209-A2.
 XX
 PD 03-DEC-1998.
 XX
 XX
 PF 29-MAY-1998; 98WO-GB001572.
 XX
 PR 31-MAY-1997; 97GB-00011148.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 XX
 PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
 XX
 DR WPI; 1999-059806/05.
 DR N-PSDB; AAV84198.
 XX
 PT New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.
 XX
 PS Disclosure; Fig 1; 44pp; English.
 XX
 CC This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC K0912 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AAV88277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
 CC an extracellular lectin-like domain. 2. Alternatively spliced forms (see
 CC AAW8266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AAW8258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 XX
 SQ Sequence 189 AA;
 Query Match 53.3%; Score 548.5; DB 2; Length 189;
 Best Local Similarity 55.6%; Pred. No. 7e-51;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
 QY 1 MADSSIVSTLELPEAPQVQDESRLKAVLHRLHSLRFAMVALGLTLVILMSLLMYQRI 60
 Db 1 MTDVSVIYMLELPTATQANDYGPQQKSSSSKSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 CCGSKDSTCSHCPCPILWTRNGSHCYFFSMKKDWNSSILKFCADKGSLLTFPDNGVK 120
 Db 61 CQGSNYSTCASCPCPDWWMKYGNHCYFFSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 QY 121 LFGYEYLGQDPFYWTGLRNDGWRWEGGPAISL-RILTNLSLQRCGAHNRGLQASCEVAL 179
 Db 121 LLQVFLSEAPFCWIGLRNNSGWRWEDGSPNFSRISNSFVQTCGAINKNGLQASCEVPL 180
 QY 180 QWICKKV 186
 Db 181 HGVCCKV 187
 RESULT 8
 AAE11759
 ID AAE11759 standard; protein; 189 AA.
 AC AAE11759;
 XX
 XX 18-DEC-2001 (first entry)
 DT
 XX Human mast cell function associated antigen (MAFA) protein.
 XX Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW

KW immunosuppressive; cytostatic.
 XX Homo sapiens.
 OS
 PN WO200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX
 DR WPI; 2001-611482/70.
 DR N-PSDB; AAD18734.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 PS Claim 10; Page 18; 49pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 XX
 SQ Sequence 189 AA;
 Query Match 53.3%; Score 548.5; DB 4; Length 189;
 Best Local Similarity 55.8%; Pred. No. 7e-51;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
 QY 1 MADSSIVSTLELPEAPQVQDESRLKAVLHRLHSLRFAMVALGLTLVILMSLLMYQRI 60
 Db 1 MTDVSVIYMLELPTATQANDYGPQQKSSSSKSCSLVAITLGLTAVLLSVLLYQWIL 60
 QY 61 CCGSKDSTCSHCPCPILWTRNGSHCYFFSMKKDWNSSILKFCADKGSLLTFPDNGVK 120
 Db 61 CQGSNYSTCASCPCPDWWMKYGNHCYFFSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
 QY 121 LFGYEYLGQDPFYWTGLRNDGWRWEGGPAISL-RILTNLSLQRCGAHNRGLQASCEVAL 179
 Db 121 LLQVFLSEAPFCWIGLRNNSGWRWEDGSPNFSRISNSFVQTCGAINKNGLQASCEVPL 180
 QY 180 QWICKKV 186
 Db 181 HGVCCKV 187
 RESULT 9
 ABG05451
 ID ABG05451 standard; protein; 843 AA.
 XX
 AC ABG05451;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #5442.

```

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS69638.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 35810; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 843 AA;
XX
Query Match 40.9%; Score 420.5; DB 4; Length 843;
Best Local Similarity 50.3%; Pred. No. 3.7e-36;
Matches 80; Conservative 26; Mismatches 52; Indels 1; Gaps 1;
QY 11 ELPEAPQVQDSRWKLVKAVLRPHLSRFAMVALGLTTLVLMQLYQRLCGSKDSTCS 70
D6 665 ELPTATQNDYGPQKSSRRSPSCVLVALAGLTLVLLSVLYQMLQGSNYSTCA 724
QY 71 HCPSPCPLWTRNGSHCYFYSMEKKDWNSSLKPCADKGSLLTFFPDNQGVKLFGEYIGQDF 130
D6 725 SCFSCPDWRWYKGNHCYFYFVEEKDWNSSLFECFLARDSHLLVITDQEMSLQLVFLSEAF 784
QY 131 YWIGLRNIDGWREGGPALSRLILTN-SLIQRCGAHRN 168
D6 785 CWIGLRNNSGMWEDGSPLNFRNTNGTIIRKRKLHKN 823
XX
RESULT 10
ABU37898
ID ABU37898 standard; protein; 191 AA.

```

```

XX AC ABU37898;
XX
XX 22-MAY-2003 (first entry)
XX
XX NOVX protein sequence SEQ ID No 42.
XX
XX Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
KW vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic;
KW antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
KW anticonvulsant; antiaddictive; analgesic; dermatological; keratolytic;
KW antiseborrheic; antirheumatic; antiarthritic; antinflammatory; anti-HIV;
KW cytostatic; antiasthmatic; antipsoriatic; hypotensive; osteopathic;
KW antulcer; anorectic; antidiabetic; antiallergic; haemostatic;
KW neuroleptic; antidepressant; antiinfertility; NOVX; human disease;
KW NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
KW parasitic infection; Alzheimer's disease; stroke; forensic biology;
KW immunogen; non-human transgenic animal; gene therapy.
XX
XX Unidentified.
XX
XX WO200281517-A2.
XX
XX 17-OCT-2002.
XX
XX 22-JAN-2002; 2002WO-US002064.
XX
XX 19-JAN-2001; 2001US-0262892P.
XX 23-JAN-2001; 2001US-0263598P.
XX 24-JAN-2001; 2001US-0263799P.
XX 25-JAN-2001; 2001US-0264117P.
XX 26-JAN-2001; 2001US-0264139P.
XX 30-JAN-2001; 2001US-0264478P.
XX 02-MAR-2001; 2001US-0263351P.
XX 14-MAR-2001; 2001US-0275927P.
XX 14-MAR-2001; 2001US-0275990P.
XX 15-MAR-2001; 2001US-0276449P.
XX 20-MAR-2001; 2001US-0277358P.
XX 23-MAR-2001; 2001US-0278151P.
XX 29-MAR-2001; 2001US-0279857P.
XX 20-APR-2001; 2001US-0285140P.
XX 20-APR-2001; 2001US-0285141P.
XX 30-APR-2001; 2001US-0287484P.
XX 17-MAY-2001; 2001US-0291701P.
XX 08-JUN-2001; 2001US-0296960P.
XX 10-JUL-2001; 2001US-0304353P.
XX 10-JUL-2001; 2001US-0304355P.
XX 12-JUL-2001; 2001US-0304886P.
XX 09-AUG-2001; 2001US-0311289P.
XX 13-AUG-2001; 2001US-0311975P.
XX 16-AUG-2001; 2001US-0312937P.
XX 18-OCT-2001; 2001US-0330227P.
XX 29-NOV-2001; 2001US-0334198P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Decristofaro MF, Padigaru M, Miller C, Tchernev V, Zhong H;
XX Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastelli L;
XX Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M;
XX Burgess CE, Eisen A, Wolenc A, Baumgartner J, Shinkets RA, Gusev V;
XX Vernet CAM, Taupier RJ, Pena C, Shenoy S, Li L, Casman S, Boidog F;
XX Fernandes E, Smithson G, Malyankar U, Tallon B, Liu X;
XX
XX WPI; 2003-058504/05.
XX N-PSDB; ABT33363.
XX
XX New polypeptides, designated as NOVX, useful for diagnosing and treating
PT infections, neurological diseases, cancer, allergy, and bone,
PT immunological, skin, renal, brain, muscle and autoimmune disorders.
XX
XX Claim 1; Page 118; 672pp; English.
XX

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CC The invention relates to a novel isolated polypeptide, designated NOVX
 CC (NOV1 - 33), consisting of a mature form of one of 61 sequences, given in
 CC the specification, or its variant, where amino acid residue(s) in the
 CC variant differ from the mature form, provided that the variant differs in
 CC not more than 15 % of the amino acids from the sequence of the mature
 CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
 CC an antibody to the polypeptides, are useful for treating or preventing a
 CC NOVX-associated disorder in humans and for treating a syndrome associated
 CC with a human disease (NOVX-associated disorder). NOVX polypeptides and
 CC the encoding nucleic acids, are useful for determining the presence of or
 CC predisposition to a disease associated with altered levels of NOVX
 CC polypeptide and polynucleotide, by measuring the level of polypeptide
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. NOVX
 CC polypeptide is also useful for identifying an agent that binds to NOVX
 CC and a cell expressing NOVX is useful for identifying an agent that
 CC modulates the expression or activity of NOVX. The antibodies and a
 CC polypeptide having 95 % sequence identity to NOVX polypeptide are useful
 CC for treating a pathological state in a mammal. The antibodies are also
 CC useful for determining the presence or amount of NOVX in a sample. NOVX
 CC polypeptides, polynucleotides and antibodies specific for the
 CC polypeptides are useful for treating or preventing disorders or syndromes
 CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
 CC infections. They can also treat disorders such as e.g., Alzheimer's
 CC disease or a stroke. The NOVX encoding nucleic acids are useful for
 CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
 CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
 CC for identifying a cell or tissue type in a biological sample, to amplify
 CC DNA sequences from very small biological samples such as tissues e.g.
 CC hair or skin or body fluids in forensic biology and as primers and probes
 CC for use in identifying and/or cloning NOVX homologues in other cell
 CC types. The NOVX proteins are useful as an immunogen to generate
 CC antibodies which are useful for diagnostically monitoring protein levels
 CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are
 CC useful for producing non-human transgenic animals which are useful for
 CC studying the function and/or activity of NOVX protein and for identifying
 CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic
 CC acids can be used in gene therapy. This sequence represents a NOVX
 CC protein of the invention

XX SQ Sequence 191 AA;

Query Match 26.0%; Score 267.5; DB 6; Length 191;
 Best Local Similarity 31.2%; Pred. No. 1.9e-20;
 Matches 59; Conservative 27; Mismatches 60; Indels 23; Gaps 4;
 Qy 12 LPEAPQVQDESRLKXAVLRPHLS-----RFAMVALGLLTVILSLMLYQRIILCCGSKDS 67
 Db 12 LPESQPFESHQRLVLLPIL-BIHVNSKSYRMYSFCLGLFTLVRSQLSLSPLECSGALSA 70
 Qy 68 TCSHCPCSPILWTRNGSHCYFFSMKDWNSLKFCDKGSLLITFPDNGVKLFGVILG 127
 Db 71 HCKICEPCPTSWLPFGGSCYFFSVFKTTWBAQGHCDASAHAAFPEDRXKVFYSVLLG 130
 Qy 128 QDFYWGILNRDGRWEGGSPALSLRLITNSLIQRCGAIHR-----NGLQASSCEVA 178
 Db 131 RCLFGIGLARVGGWRQVAPGTQI-----DAPAVGQACFCQBSISGLPASELRLE 181
 Qy 179 LQWICKKVL 187
 Db 182 KWHCSKTL 190

RESULT 11

AAW88267
 ID AAW88267 standard; protein; 99 AA.

XX AC AAW88267;

XX DT 29-MAR-1999 (first entry)

XX DE Human MAFa splice variant huMAFA(E3/4-).

KW Mast cell function-associated antigen; MAFa; huMAFA(E3/4-);
 KW splice variant; human; inflammation; allergy; asthma;
 KW rheumatoid arthritis; tumour; therapy.

OS Homo sapiens.

PN WO9854209-A2.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB001572.

XX PR 31-MAY-1997; 97GB-00011148.

XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX DR WPI; 1999-059806/05.

XX DR N-PSDB; AAV84200.

XX PT New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.

XX PS Disclosure; Fig 3; 44pp; English.

XX CC This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
 CC like domain of human MAFa (see AAW88265) but retains the intracellular
 CC and transmembrane domains as well as the extracellular C-terminal tail.
 CC Truncated MAFa polypeptides including huMAFA(E3/4-), and polynucleotides
 CC encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
 CC 72), can be used in compositions for the treatment of
 CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and
 CC asthma), or tumour growth

XX SQ Sequence 99 AA;

Query Match 21.6%; Score 222.5; DB 2; Length 99;
 Best Local Similarity 30.1%; Pred. No. 5.9e-16;
 Matches 56; Conservative 13; Mismatches 28; Indels 89; Gaps 1;
 Qy 1 MADSIYSTELEPEAPQVQDESRLKXAVLRPHLSRFAMVALGLLTVILSLMLYQRIIL 60
 Db 1 MTDSVIYSMLEPTATQADYGFQPKSSSRFSCSCLVAIALGLLTVILSLVLLYQWIL 60
 Qy 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFFSMKDWNSLKFCDKGSLLITFPDNGVK 120
 Db 61 CCG-----
 Qy 121 LFGEYLQDFYTWIGLRNIDGRWEGGSPALSLRLITNSLIQRCGAIHRNGLQASSCEVALQ 180
 Db 64 -----ISSNSFVTCGATKNGLQASSCEVPLH 91
 Qy 181 WICKKV 186
 Db 92 WICKKV 97

RESULT 12

AAW85594
 ID AAW85594 standard; protein; 257 AA.

XX AC AAW85594;

XX DT 17-OCT-2003 (revised)

XX DT 02-MAR-1999 (first entry)

XX DE Chicken 17.5.3 protein.

XX KW lectin; carbohydrate; binding; agglutination; selectin; receptor;

KW calcium dependent binding; treatment; cancer; detection; identification;
 KW CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
 OS Gallus gallus.
 XX WO9849306-A1.
 PN XX
 XX 05-NOV-1998.
 PD XX
 PF 29-APR-1998; 98WO-US008791.
 XX XX
 PR 29-APR-1997; 97US-00846523.
 XX XX
 PA (INCY-) INCYTE PHARM INC.
 XX XX
 PI Bandman O, Shah P;
 XX XX
 DR WPI; 1999-024060/02.
 DR N-PSDB; AAV83109.
 XX XX

XX New human C-type lectin and related nucleic acid, vectors, transformed
 PT cells - antibodies, agonists and antagonists, for diagnosis, prevention
 PT and treatment of cancers.
 XX XX

PS Example 3; Page 48-49; 64pp; English.
 XX XX
 CC Chicken 17.5.3 protein shows homology with the human CTL-1 protein.
 CC Recombinant cells containing expression vectors comprising the CTL-1
 CC coding sequence can be used to produce recombinant CTL-1 which is useful
 CC for raising Ab and to screen for specific binding agents. Binding agents
 CC which are antagonists of CTL-1 can be used to treat or prevent cancer,
 CC e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are
 CC associated with overexpression of CTL-1. Fragments of this sequence are
 CC used to diagnose these conditions, as probes or primers in usual
 CC hybridisation and/or amplification assays, or for gene mapping, while
 CC complements of this sequence, antisense or ribozyme sequences are used to
 CC treat or prevent the aforementioned cancers also. Ab are used directly as
 CC antagonists or for delivery of therapeutic agents to cells that express
 CC CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
 CC also a transmembrane domain, but no secretory signal. CTL-1 also shows
 CC homology with human CD69 (AAW85593), and mouse CD69 (AAW85595) proteins.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX XX

SQ Sequence 257 AA;
 Query Match 17.7%; Score 182; DB 2; Length 257;
 Best Local Similarity 28.7%; Pred. No. 5.1e-11;
 Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;
 QY 32 RPHLSRFAMVALG----LLTVILMSLLMYQRIKCGSKDSTCSHCPCPILWTRNGSHCY 87
 Db RQNRRLVLCVALSAVPCMLVLAVAVILQRPSC--SPRPFSHV--CFNAWVGFGKCY 141
 QY 88 YFSMEKDWNSSLKFCADKSGHLLTFPPNQGVKLFGEYLGQDFYWGILNRIDG---WWE 144
 Db 142 YFSTESDWNSSRHHCHRLGSLATLDTKEEMFLQYQRPADRWIGLHRAEGDEHTWA 201
 QY 145 GGPALSLRILTNLI-----QRCGAIRHNGLOASSCEVALQWICKK 185
 Db 202 DGSA-----FTNRPVFEELGGRCAYLNGDISALCHSEKFWCSR 243

RESULT 13
 AAW64791
 ID AAW64791 standard; protein; 179 AA.
 XX XX
 AC AAW64791;
 XX XX
 DT 23-NOV-1998 (first entry)
 XX XX
 DE Human Kp43 protein.
 XX XX
 KW Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor;

KW cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
 XX Homo sapiens.
 XX US5811284-A.
 PN XX
 XX 22-SEP-1998.
 PD XX
 PF 20-MAY-1996; 96US-00650578.
 XX XX
 PR 29-DEC-1993; 93US-00175339.
 XX XX
 PA (SCHE) SCHERING CORP.
 PA (LOPE/) LOPEZ-BOTET M.
 PA (BELT/) BELTRAN J A.
 XX XX
 PI Lanier LL, Chang C, Lopez-Botet M, Beltran JA, Phillips JH;
 XX XX
 DR WPI; 1998-530877/45.
 DR N-PSDB; AAV46476.
 XX XX
 PT DNA encoding natural killer cell surface antigen Kp43 - and transformed
 PT cells for producing recombinant Kp43.
 XX XX
 PS Claim 1; Col 31-32; 17pp; English.
 XX XX
 CC This sequence represents a novel human natural killer (NK) cell surface
 CC antigen, Kp43. This sequence can be used in a method resulting in the
 CC production of recombinant protein expressed by NK and T cells, which may
 CC inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or
 CC autoimmune diseases, or may be used to produce antibodies for diagnostic
 CC or therapeutic use
 XX XX
 SQ Sequence 179 AA;

Query Match 17.3%; Score 178.5; DB 2; Length 179;
 Best Local Similarity 31.8%; Pred. No. 7.5e-11;
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
 QY 44 GLLIVILMSLLMYQRIKCGS-----KSTCSHCPCPILWTRNGS 84
 Db 14 GTLGIICLSMATILGILKNSFTKLSTEPATPGNIBLQKSDC--C-SCQEKWVG YRC 70
 QY 85 HCYVFSMEKDWNSSLKFCADKSGHLLTFPPNQGVKLFGEYLGQDFYWGILNRIDG---GW 141
 Db 71 NCYFISSEOKTWNESRHLCSQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
 QY 142 RWEGGPALSLRILTN---SLIQRCAIRHNG-LOASSCEVALQWICKKVL 187
 Db 129 LWENGSAISQYLFPSFETFKNCIAYNPNGNALDESCEDKNRYICKQL 178

RESULT 14
 AAW40222
 ID AAW40222 standard; peptide; 179 AA.
 XX XX
 AC AAW40222;
 XX XX
 DT 07-JUL-1998 (first entry)
 XX XX
 DE CD94.
 XX XX
 KW TMAH; apoptosis; osteoarthritis; diagnosis; treatment.
 XX XX
 OS Homo sapiens.
 XX XX
 PN WO9804585-A2.
 XX XX
 PD 05-FEB-1998.
 XX XX
 PF 22-JUL-1997; 97WO-US013077.
 XX XX
 PR 31-JUL-1996; 96US-00690095.

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XX PA (INCY-) INCYTE PHARM INC.
XX PI Hillman JL, Au-Young J, Goli SK;
XX SK WPI; 1998-130617/12.
XX DR Human macrophage antigen - used for decreasing apoptosis associated with
XX PT osteoarthritis.
XX PT Human macrophage antigen - used for decreasing apoptosis associated with
XX PT osteoarthritis.
XX PS Disclosure; Page 47; 58pp; English.
XX CC The type II integral membrane proteins (AAW40219-W40221) and CD94
XX CC (AAW40222) form a group which has 20% homology with the human macrophage
XX CC antigen (TMAH) (AAW40215). The homology which TMAH shares with this group
XX CC includes a series of disulphide residues. The structural homology between
XX CC the peptides provides information on the structural and physical
XX CC properties of both the TMAH gene and protein. This is used in the
XX CC development of TMAH as a diagnostic tool and as a method of treating
XX CC diseases associated with expression of TMAH
XX CC
XX SQ Sequence 179 AA;
XX
Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 7.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIICLSMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYFMSMEKDMNSSLKFCADKSGHLLTFPDNQGVKLFGEYLGDQFWWIGLRNID---GW 141
Db 71 NCYFISSEQKTWNEHRHLCAQSKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCGAHRNG-LQASCEVALQWICKKVL 187
Db 129 LWENGSAQLPFPFETFTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 15
ADE76965
ID ADE76965 standard; protein; 179 AA.
XX AC ADE76965;
XX DT 29-JAN-2004 (first entry)
XX DE Human protein expressed in a liver disorder #36.
XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
XX KW tumour; liver; inflammatory disorder; immune response disorder;
XX KW high-throughput screening; differential gene expression; gene therapy.
XX OS Homo sapiens.
XX PN US2003108871-A1.
XX PD 12-JUN-2003.
XX PF 30-JUL-2001; 2001US-00919039.
XX PR 28-JUL-2000; 2000US-0222113P.
XX PA (KASE/) KASER M R.
XX PI Kaser MR;
XX DR WPI; 2004-031227/03.
XX DR N-PSDB; ADE76964.
XX PT Composition comprising several cDNAs that are differentially expressed in
XX PT treated human C3A liver cell cultures, useful for treating liver

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PT disorders.
XX Claim 1; SEQ ID NO 130; 41pp; English.
XX
XX The invention relates to a composition comprising several cDNAs that are
XX differentially expressed in a liver disorder. The composition is useful
XX for treating liver disorder such as hyperlipidaemia, hypertension, type
XX II diabetes, tumours of the liver and disorders of the inflammatory and
XX immune response. The composition is useful for a high-throughput method
XX of screening several molecules or compounds to identify a ligand which
XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX high-throughput method for using a protein to screen several molecules or
XX compounds to identify at least one ligand which specifically binds the
XX protein which involves combining the protein encoded by the cDNA with
XX several of molecules or compounds under conditions to allow specific
XX binding, and detecting specific binding between the protein and a
XX molecule or compound, therefore identifying a ligand which specifically
XX binds the protein. The composition is useful for detecting and
XX quantifying differential gene expression, can be used in gene therapy, to
XX formulate prognosis and to design a treatment regimen and to monitor the
XX efficacy of treatment. The present sequence represents the amino acid
XX sequence of a protein encoded by a cDNA differentially expressed in a
XX liver disorder.
XX
XX SQ Sequence 179 AA;
XX
Query Match 17.3%; Score 178.5; DB 8; Length 179;
Best Local Similarity 31.8%; Pred. No. 7.5e-11;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;
QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIICLSMATLIGILLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYFMSMEKDMNSSLKFCADKSGHLLTFPDNQGVKLFGEYLGDQFWWIGLRNID---GW 141
Db 71 NCYFISSEQKTWNEHRHLCAQSKSLQLQNTDELDFMSS--SQQFYWIGLSYEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCGAHRNG-LQASCEVALQWICKKVL 187
Db 129 LWENGSAQLPFPFETFTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

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OM protein - protein search, using sw model

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(without alignments)
1464.718 Million cell updates/sec

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Perfect score: 1029
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	188	9	US-09-811-367B-3
2	838	81.4	188	9	US-09-811-367B-5
3	568.5	55.2	189	14	US-10-207-655-196
4	548.5	53.3	189	9	US-09-811-367B-1
5	182	17.7	257	14	US-10-179-528-4
6	178.5	17.3	179	10	US-09-919-039-130
7	178.5	17.3	179	15	US-10-335-009-10
8	173.5	16.9	199	10	US-09-284-320-86
9	173.5	16.9	199	14	US-10-207-655-182
10	173.5	16.9	199	14	US-10-179-528-3
11	173.5	16.9	199	15	US-10-379-127-26
12	171.5	16.7	231	16	US-10-451-843-1
13	170	16.5	546	12	US-10-072-012-158
14	170	16.5	549	12	US-10-072-012-160
15	168	16.3	199	14	US-10-179-528-7

16	166.5	16.2	198	9	US-09-764-870-470	Sequence 470, App
17	166.5	16.2	198	14	US-10-125-540-470	Sequence 470, App
18	166.5	16.2	203	9	US-09-764-870-309	Sequence 309, App
19	166.5	16.2	203	14	US-10-125-540-309	Sequence 309, App
20	166.5	16.2	345	12	US-10-262-839-94	Sequence 94, Appl
21	164.5	16.0	225	15	US-10-379-127-25	Sequence 25, Appl
22	163.5	15.9	191	15	US-10-335-009-2	Sequence 2, Appl
23	163.5	15.9	191	15	US-10-379-127-23	Sequence 23, Appl
24	162.5	15.8	251	9	US-09-764-870-300	Sequence 300, App
25	162.5	15.8	251	9	US-10-125-540-300	Sequence 300, App
26	160.5	15.6	251	13	US-10-114-893-22	Sequence 22, Appl
27	160.5	15.6	265	9	US-09-764-870-307	Sequence 307, App
28	160.5	15.6	265	14	US-10-125-540-307	Sequence 307, App
29	160.5	15.6	275	15	US-10-161-493-20	Sequence 20, Appl
30	156	15.2	182	9	US-09-764-870-310	Sequence 310, App
31	156	15.2	182	14	US-10-125-540-310	Sequence 310, App
32	156	15.2	268	15	US-10-161-493-22	Sequence 22, Appl
33	154	15.0	165	10	US-09-759-130B-98	Sequence 98, Appl
34	154	15.0	165	16	US-10-741-790-98	Sequence 88, Appl
35	154	15.0	190	10	US-09-759-130B-88	Sequence 88, Appl
36	154	15.0	190	16	US-10-741-790-88	Sequence 14, Appl
37	154	15.0	190	16	US-10-775-640-14	Sequence 4, Appl
38	153	14.9	316	9	US-09-862-802-4	Sequence 4, Appl
39	152.5	14.8	319	15	US-10-138-588-90	Sequence 90, Appl
40	152.5	14.8	1479	12	US-09-918-715-305	Sequence 305, App
41	152	14.8	189	9	US-09-764-870-487	Sequence 487, App
42	152	14.8	189	14	US-10-125-540-487	Sequence 487, App
43	151.5	14.7	399	16	US-10-451-459-2	Sequence 2, Appl
44	151	14.7	132	15	US-10-335-009-4	Sequence 4, Appl
45	149.5	14.5	1479	12	US-09-918-715-238	Sequence 238, App

ALIGNMENTS

RESULT 1

US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811.367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match	100.0%	Score 1029;	DB 9;	Length 188;
Best Local Similarity	100.0%	Pred. No. 7.9e-101;		
Matches 188;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MADSSYSTLELPEAPQVDSRWKLVKAVLRPHLSRFAMVALGTLTIVLSLMYQRIIL	60	
Db	1	MADSSYSTLELPEAPQVDSRWKLVKAVLRPHLSRFAMVALGTLTIVLSLMYQRIIL	60	
QY	61	CGGSKDSTCSHCPCPILWTRNGSCYFYFSMEKDDNSLKFCDKDGSHLLTFPDNQGVK	120	
Db	61	CGGSKDSTCSHCPCPILWTRNGSCYFYFSMEKDDNSLKFCDKDGSHLLTFPDNQGVK	120	
QY	121	LFGEYLGQDFYWIGLRNIDGWRWEGGPPALSRLILNLSIQRCAIHRNGLQASCEVALQ	180	
Db	121	LFGEYLGQDFYWIGLRNIDGWRWEGGPPALSRLILNLSIQRCAIHRNGLQASCEVALQ	180	

```
QY 181 WICKKVL 188
Db 181 WICKKVL 188

RESULT 2
US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match 81.4%; Score 838; DB 9; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.4e-80;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSIYSTLELPEAPQVQDSRWKLVKAVLHRPHLSRFAMVALGLLTIVILMSLLMYQRI 60
Db 1 MADNSSIYSTLELPEAPRQDQSRWKVAVLHRPCVSYLVAMVALGLLTIVILMSLLMYQRI 60

QY 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFFPDNGVK 120
Db 61 CCGSGFGMCQSCRCPNLMWRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFFPDNGVN 120

QY 121 LFGEYLGQDFYWGILNRNIDGWRWEGGPALES-LRILTNLSIORCGAIHRNGLOASSCEVAL 179
Db 121 LFQEVGDFYWGILNRNIDGWRWEGGPALES-LRILTNLSIORCGAIHRNGLOASSCEVAL 180

QY 181 WICKKVL 187
Db 181 WICKKVL 187

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match 55.2%; Score 568.5; DB 14; Length 189;
Best Local Similarity 57.2%; Pred. No. 5.7e-52;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 181 WICKKVL 188
Db 181 WICKKVL 188

RESULT 4
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1

Query Match 53.3%; Score 548.5; DB 9; Length 189;
Best Local Similarity 55.6%; Pred. No. 7.5e-50;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSIYSTLELPEAPQVQDSRWKLVKAVLHRPHLSRFAMVALGLLTIVILMSLLMYQRI 60
Db 1 MTDSVIYSMLELPTATQANDYGFQKSSSSKPSCLVAITLGLTAVLLSVLLYQWIL 60

QY 61 CCGSKDSTCSHCPCSPILWTRNGSHCYFYSMEKKDWNSSLKFCADKGSLLTFFPDNGVK 120
Db 61 CCGSNYSTCASCPCSPDRWKYGNHCYFYSVEEKDWNSSLEFLARDSHLLVITDNOEMS 120

QY 121 LFGEYLGQDFYWGILNRNIDGWRWEGGPALES-LRILTNLSIORCGAIHRNGLOASSCEVAL 179
Db 121 LLQVFLSEAFWCWIGLNRNNSGWRWEDGSPLNFSRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 180 QWICKKV 186
Db 181 HWCKKV 187

RESULT 5
US-10-179-528-4
; Sequence 4, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
```

OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CDI
US-09-919-039-130

Query Match 17.3%; Score 178.5; DB 10; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.3e-10; Indels 31; Gaps 7;
Matches 54; Conservative 17; Mismatches 68

QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
DB 14 GTLGIIICLSMATLGLLLKNSFTKLSIBPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYYFSMEKKDWNSSLKFCADKSHLLTTPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNEGRHLCSQKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCAIHRNG-LOASSCEVALQWICKVYL 187
DB 129 LWENGSAISQYLFPSFETNTKNCIAYNPNGNALDESCEDKRYICKQOL 178

RESULT 7
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Porunelloor, Mathew A.
; TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469687-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match 17.3%; Score 178.5; DB 15; Length 179;
Best Local Similarity 31.8%; Pred. No. 1.3e-10;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
DB 14 GTLGIIICLSMATLGLLLKNSFTKLSIBPAFTPGPNIELQKSDC--C-SCQEKWVGRC 70
QY 85 HCYYFSMEKKDWNSSLKFCADKSHLLTTPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNEGRHLCSQKSLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSRLITN---SLIQRCAIHRNG-LOASSCEVALQWICKVYL 187
DB 129 LWENGSAISQYLFPSFETNTKNCIAYNPNGNALDESCEDKRYICKQOL 178

RESULT 8
US-09-284-320-86
; Sequence 86, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,528
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0281 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 505325
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-179-528-4

Query Match 17.7%; Score 182; DB 14; Length 257;
Best Local Similarity 28.7%; Pred. No. 8.3e-11;
Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;

QY 32 RPHLSRSMYALG---LLTVILMSLLMYQRIILCCGSKDSCTSCSPILWTRNGSHCY 87
DB 86 QONRRRLVCVALSAPVCMVLVALVAVILQRPSC--SPRPFSHV--CFNANWVGQKCY 141
QY 88 YFSMEKKDWNSSLKFCADKSHLLTTPDNQGVKLFGEYLGQDFYWGILRNIDG---WRWE 144
DB 142 YFSDTESDWNSSRHRCHRLGASLATLDTKEEMEFMLQYQREADRWIGLHRAEGDEHTWA 201
QY 145 GGPALSRLITNSLI-----QRCAIHRNGIQAASSCEVALQWICKK 185
DB 202 DGS-----FTNRPVFEIIRGGRCAYLNGDGISSALCHSEKFWVCSSR 243

RESULT 6
US-09-919-039-130
; Sequence 130, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 86
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-86

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Query Match	16.9%;	Score 173.5;	DB 10;	Length 199;
Best Local Similarity	23.8%;	Pred. No. 4.8e-10;		
Matches	48;	Conservative 36;	Mismatches 83;	Indels 35; Gaps 8;
QY	3	DSISYETLELPEAPQVQDESRLKKAVLHPEHLR-----FAMVALGELLVILM	51	
Db	11	NSSLH-----PRSGQENDAT-----SPHSTRHGSGFQPVLCAMNVVFITILII	56	
QY	52	SL--LMYQRIILCGSKDSTC---SHCPSPFILWTRNGSHCHYFSEMEKKNWSLKFCADK	106	
Db	57	ALIALSVGQYNCPGQYTFSPSPSDSHVSSCSDEDVVGQYKCYFISTVKRSWTSQAQACSEH	116	
QY	107	GSHLLTFPDNQVKLFGELYGDQFYWIGLRLNDG--WRWEGGPALSRLI-LTNSLIQRCG	163	
Db	117	GATLAVIDSEKDNFLKRYAGREHHVGLKPEGHPKWSNGKEFNWFWNTGS---DKCV	174	
QY	164	AHRNGLQASSCEVALQWICKK	185	
Db	175	FLKNTVSVSMECEKNLYWICNK	196	

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RESULT 9
US-10-207-655-182
; Sequence 182, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 182
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-10-207-655-182

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Query Match      16.9%; Score 173.5; DB 14; Length 199;
Best Local Similarity 23.8%; Pred. No. 4.8e-10;
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

      3 DSSYSTLEPEAPOQDESRLKXAVLRPHLSR-----FAMVALGLLTWILM 51
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
      11 NSSUH-----PESGQNDAT-----SPHFSTRHESGQVPVLCAWMNVFITLLI 56
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

      52 SL--LMYQRLCCSGSDSTC---SHCPSPILWTNRNGSHCYFYSEKKDWNSSLKFCADK 106
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

      57 ALIALSGVQNCPGQYTFSPMPSDSHVSSCSGDWDVGQYQKCYFISTVKRSTWTAQACSEH 116
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

      107 GSHLLTFPDNQGYKLFGEYLGDQFWIGLNRIDG--WRWEGGPALSLRL-LTNSLIQRQC 163
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

      117 GATLAVIDSEKWNFLKRYAGREEHWGLKEPQGHFMKWSNGKGFNNWFNTGS--DKCV 174
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

      164 AIHRNGLOASSCEVALQWICKK 185
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

      175 FLKNTVESSMECEKNLYWICNK 196
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

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RESULT 10
US-10-179-528-3
Sequence 3, Application US/10179528
Publication No. US20030166136A1

```

1 GENERAL INFORMATION:
2 APPLICANT: Bandman, Olga
3 Shah, Purvi
4 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
5 NUMBER OF SEQUENCES: 7
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Incyte Pharmaceuticals, Inc.
8 STREET: 3174 Porter Drive
9 CITY: Palo Alto
10 STATE: CA
11 COUNTRY: USA
12 ZIP: 94304
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Diskette
15 COMPUTER: IBM Compatible
16 OPERATING SYSTEM: DOS
17 SOFTWARE: Fast-Seq for Windows Version 2.0
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/10/179,528
20 FILING DATE: 24-Jun-2002
21 CLASSIFICATION: <Unknown>
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US/08/846,523
24 FILING DATE: <Unknown>
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Billings, Lucy J
27 REGISTRATION NUMBER: 36,749
28 REFERENCE/DOCKET NUMBER: PF-0281 US
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 415-855-0555
31 TELEFAX: 415-845-4166
32 TELEX: <Unknown>
33 INFORMATION FOR SEQ ID NO: 3:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 199 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 IMMEDIATE SOURCE:
40 LIBRARY: GenBank
41 CLONE: 291898
42 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
43 US-10-179-528-3

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Query Match	16.9%;	Score 173.5;	DB 14;	Length 199;
Best Local Similarity	23.8%;	Pred. No. 4.9e-10;		
Matches	48;	Conservative 36;	Mismatches 83;	Indels 35; Gaps 8;
QY	3	DSISYLTLEPAQYQDERSMKLXAVLRPHLSR-----FAMVALGLLTIVILM	51	
Db	11	NASLH-----PRGQNDAT-----SPHSTRHGSGFQPVLCAMNVVFTILII	56	
QY	52	SL--LMYQRIILCGSKDSTC---SHCPSPFILWTRNGSHCYFSEMKDWNSSLKFCADK	106	
Db	57	ALIALSVGQYNCPGQYTFSPMSDSDSHVSSCSDEWVGQYKCYFISTVKRSWTSQAQACSEH	116	
QY	107	GSHLLTFPDNQVKLGEYLQGFYWGHRNIDG--WRWEGGPALSRI-LTNSLIQRCG	163	
Db	117	GAFLAVITSEKDMNFTKRYAGREEHWMLKCBPGHPKWSNGKEFNNWNVFTGS--DKCV	174	
QY	164	AHRNGLQASCEVALOWICKK	185	
Db	175	FLKNTFVSSMECEKNLYIENK	196	

RESULT 11
US-10-379-127-26
; Sequence 26, Application US/10379127
; Publication No. US2004000552A1
; GENERAL INFORMATION:
; APPLICANT: Emgate, Peter C.R.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Goodman, Ryle

QY 137 NIDG-WRGGPALSILRLTSLIQRCA-----IHRNG-----LQAS---SC 175
Db 477 GEGSWRGTDGTFP-----NAAQNKGFEKNSDNWRHKNQGTCVGIQQKWNDMTC 539

QY 176 EVALQWICKK 185
Db 530 DTPYOWVCCK 539

RESULT 14

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US-10-072-012-160
; Sequence 160, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Sytsek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072012

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SEE REFERENCE: 21102-230
CURRENT APPLICATION NUMBER: US/10/072.012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514
 ; PRIOR FILING DATE: 2001-03-27

; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 50/365 513

; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31

EXPIRATION DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,395

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/266,406
 ; PRIOR FILING DATE: 2001-03-08

; PRIOR FILING DATE: 2001-02-02
 : PRIOR APPLICATION NUMBER: 60/266 767

: PRIOR FILING DATE: 2007-02-05
 : PRIOR APPLICATION NUMBER: 60/266,767

;; PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

;; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07

;; PRIOR APPLICATION NUMBER: 60/267,459

;; PRIOR FILING DATE: 2001-02-08
: Remaining Prior Application date: 2001-02-08

REMAINING PRIOR APPLICATION DATA REMOVED
NUMBER OF SEQ ID NOS: 1391

; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 160

LENGTH: 549

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-160

Query Match 16 5% Score 170.

Query Match	16.3%	Score 170;
Best Local Similarity	30.0%	Pred. No.

[illegible]

	Matches	39; Conservative	17; Mismatches	44; Indels	30; Gaps	6
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Db	420	WKFNNGSLIYFSSVKKSHHRAEQFCVQGAHLASVASKEEQAFIVFTSKVYIWIGLTDR	479			
Qy	137	NIDG--WRWEGGPALSLRLTNSLTQRCGA-----IHRNG-----LQAS-----SC	175			
Db	480	GTEGSRWWTGDTGTFP-----NAAQNGFWFEKNGQDNWRHKNGQTEPCVQLQQRWMDTC	532			
Qy	176	EVALQWICKK	185			
Db	533	DTPIYQWYCKK	542			

RESULT 15

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US-10-179-528-7
; Sequence 7, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
;           Shah, Purvi
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 584907
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-179-528-7

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[illegible]

Db 97 YPESITTKSWALQORSCSEDAATLAVIDSEKDMTFLKRYSGELEHHWIGLKNEANQTKWA 156

Qy 145 GGPAL-SLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185

Db 157 NGKEFNSWFENLTGS--GRCVSVNHKNVTAVDCEANFHWVCSK 196

Search completed: August 10, 2004, 16:32:37
Job time : 41.2619 secs

mis Page Blank (uspio)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.6407 Seconds
(without alignments)
662.924 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSIVSTLELPEAPQVQD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	838	81.4	188	3	US-08-722-126A-5
2	838	81.4	188	5	PCT-US95-04258-5
3	551	53.5	114	3	US-08-722-126A-6
4	551	53.5	114	5	PCT-US95-04258-6
5	267	25.9	76	4	US-09-531-056A-23
6	178.5	17.3	179	1	US-08-690-095-9
7	178.5	17.3	179	2	US-08-650-578-2
8	178.5	17.3	179	2	US-08-688-342-3
9	178.5	17.3	179	2	US-09-113-789-3
10	178.5	17.3	179	3	US-09-113-789-9
11	173.5	16.9	199	5	PCT-US93-10418-2
12	168	16.3	199	5	PCT-US93-10418-4
13	164.5	16.0	225	2	US-08-738-462-2
14	164.5	16.0	225	5	PCT-US94-07587-2
15	163.5	15.9	191	4	US-09-531-056A-6
16	160.5	15.6	231	1	US-08-690-095-6
17	160.5	15.6	231	3	US-09-113-789-6
18	160.5	15.6	231	3	US-08-543-246B-6
19	160.5	15.6	231	3	US-08-543-246B-23
20	154	15.0	190	4	US-09-127-946-14
21	153	14.9	316	3	US-09-111-470-4
22	152.5	14.8	1479	3	US-08-840-062-2
23	152	14.8	122	3	US-08-722-126A-9
24	152	14.8	122	5	PCT-US95-04258-9
25	152	14.8	215	1	US-08-690-095-7
26	152	14.8	215	3	US-09-113-789-7
27	152	14.8	215	3	US-08-543-246B-16

28 152 14.8 215 3 US-08-543-246B-22
29 151 14.7 233 1 US-08-690-095-8
30 151 14.7 233 3 US-09-113-789-8
31 151 14.7 233 3 US-08-543-246B-2
32 151 14.7 233 3 US-08-543-246B-21
33 151 14.7 1487 3 US-08-840-062-7
34 150.5 14.6 115 3 US-08-722-126A-8
35 150.5 14.6 115 5 PCT-US95-04258-8
36 150 14.6 328 4 US-09-531-056A-13
37 149 14.5 404 4 US-09-517-605-2
38 148 14.4 194 4 US-09-531-056A-2
39 147.5 14.3 273 3 US-09-111-470-10
40 147.5 14.3 292 2 US-08-688-342-4
41 147.5 14.3 292 2 US-09-113-788-4
42 146 14.2 135 3 US-08-543-246B-19
43 145 14.1 173 4 US-09-531-056A-4
44 144 14.0 216 3 US-08-543-246B-9
45 144 14.0 216 3 US-08-543-246B-24

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-5
Query Match 81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.8e-86;

Query Match 81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.8e-86;

	Matches	151;	Conservative	15;	Mismatches	21;	Indels	0;	Gaps	0;
Qy	1	MADSSIYSTLLELPAPQVQDES	RKWLKAVLHRLPHLSRFAMVALGLLT	VILMSLLMYORIL	60					
Dd	1	MADNSIYSTLLELPAPRVQDSDS	RWKVKAVLHRLPCVSYLVMVALGLLT	VILMSLLLYQRTL	60					
Qy	61	CCGSKDSTCSHCPCPILWTRNGSHCYFF	SMEKKDWNSSLKFCADKGSHLLT	TFPDNOGVK	120					
Dd	61	CCGSKGPMQCSCSPNLWRNGSHCYFF	SMEKRDNSSLKFCADKGSHLLT	TFPDNOGVN	120					
Qy	121	LFGYLGQDFWIGLRINDGWRWEGGPALSLRILT	NSLIORCGAIHRNGLQASCEVALQ	180						
Dd	121	LFQEYVGEDFWIGLRIDGWREDGPALSLSILSN	SVVQCKGTIHRCGLHASSCEVALQ	180						
Qy	181	WICKKVL	187							
Dd	181	WICEKVL	187							

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1 RESULT 2
2 PCT-US95-04258-5
3 Sequence 5, Application PC/TUS9504258
4 GENERAL INFORMATION:
5 APPLICANT:
6 TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
7 FUNCTION-ASSOCIATED ANTIGEN (MAFA)
8 TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
9 NUMBER OF SEQUENCES: 10
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: BROWDY AND NEIMARK
12 STREET: 419 Seventh Street, N.W., Suite 300
13 CITY: Washington
14 STATE: D.C.
15 COUNTRY: USA
16 ZIP: 20004
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US95/04258
24 FILING DATE: 06-APR-1995
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: IL 109257
27 FILING DATE: 08-APR-1994
28 ATTORNEY/AGENT INFORMATION:
29 NAME: BROWDY, Roger L.
30 REGISTRATION NUMBER: 25,618
31 REFERENCE/POCKET NUMBER: PECHT-1 PCT
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 202-628-5197
34 TELEFAX: 202-737-3528
35 TELEX: 248633
36 INFORMATION FOR SEQ ID NO: 5:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 188 amino acids
39 TYPE: amino acid
40 TOPOLOGY: linear
41 MOLECULE TYPE: protein
42 PCT-US95-04258-5

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QY      121 LFGEYLGDQFYWIGLRNIDGWRWEGGPALSLRIILTNLSLIORCGATHRRGLQASSCEVALQ 180
Db      121 LFEIYGVEDFYWIGLRDIDGWRWDGPALSLILSNVYVKCGTIHRCGLHASSCEVALQ 180
QY      181 WICKKVL 187
Db      181 WICEKVL 187
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        |||:||
RESULT 3
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAPA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-6

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RESULT 4
PCT-US95-04258-6

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; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-6

Query Match 53.5%; Score 551; DB 5; Length 114;
Best Local Similarity 84.1%; Pred. No. 2e-54; Indels 0; Gaps 0;
Matches 95; Conservative 9; Mismatches 9;

QY 75 CPILWTRNGSHCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYLGQDFYWG 134
Db 1 CPNLWNRNGSHCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLVFQEVYGVDFYWG 60

QY 135 LRNIDGWRWEGGPAISLRILTNLSLQRCGAIHRNGLQASCEVALQWICKVL 187
Db 61 LRIDGWRWEGGPAISLRILTNLSVYQCGTIHROGLHASCEVALQWICKVL 113

RESULT 5
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531.056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
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Query Match 25.9%; Score 267; DB 4; Length 76;
Best Local Similarity 59.5%; Pred. No. 1.2e-22;
Matches 44; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 73 PSCPILWTRNGSHCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYLGQDFYWG 132
Db 1 PSCPDRMKYGNHCYFYSVEEKDWNSLKFCLARDSHLLVITDQEMSLQVFLSEAFW 60

QY 133 IGLRNIDGWRWEGG 146
Db 61 IGLRNKSGWRWEDG 74

RESULT 6
US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-08-690-095-9

Query Match 17.3%; Score 178.5; DB 1; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLTIVILMSLLMYQRIILCCGS-----KSTCSHCSPCILWTRNGS 84
Db 14 GTLGIICLSMATLIGILLKNSFTKLSTIEPAFTPGPNIELQKSDC--C-SCQKQWVGRC 70

QY 85 HCYFYSMEKDWNSLKFCDKSGHLLTFPDNQGKLFGEYLGQDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128

QY 142 RWEGGPAISLRILTN---SLIQRCGAIHRNG-LQASCEVALQWICKVL 187
Db 129 LWENGSAISOYLFSPSPETFTKNCIAYPNGNALDESKDKRYICKQQL 178
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RESULT 7
US-08-650-578-2
; Sequence 2, Application US/08650578
; Patent No. 5811284
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Aramburu Beltran, Jose
; APPLICANT: Lopez-Botet, Miguel
; APPLICANT: Phillips Jr., Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; RELATED REAGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-578-2

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIICCGS-----KDTSCSHCPSCPILWTRNGS 84
DB 14 GTLGICLSMATLIGLLKNSFTKLSIEPAFTPGNIELQKSDC--C-SCQEKWGVYRC 70
QY 85 HCYFSEMEKDWNSLSKFCADKGSLLTTPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNSRHLCAQSKSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSLRLTN---SLIQRGCAIHRNG-LQASCEVALQWICKVYL 187
DB 129 LWENGSAISQVLFPSFETFKNCIAYNPNGNALDESCEDCKNRYICKQQL 178

RESULT 8
US-08-688-342-3
; Sequence 3, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
```

```
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-08-688-342-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

QY 44 GLLTVILMSLLMYQRIICCGS-----KDTSCSHCPSCPILWTRNGS 84
DB 14 GTLGICLSMATLIGLLKNSFTKLSIEPAFTPGNIELQKSDC--C-SCQEKWGVYRC 70
QY 85 HCYFSEMEKDWNSLSKFCADKGSLLTTPDNQGVKLFGEYLGQDFYWGILRNID---GW 141
DB 71 NCYFISSEQKTWNSRHLCAQSKSLLQLQNTDELDFMSS--SQQFYWIGLSYSEHTAW 128
QY 142 RWEGGPALSLRLTN---SLIQRGCAIHRNG-LQASCEVALQWICKVYL 187
DB 129 LWENGSAISQVLFPSFETFKNCIAYNPNGNALDESCEDCKNRYICKQQL 178

RESULT 9
US-09-113-788-3
; Sequence 3, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,788
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/688,342
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098616
; US-09-113-788-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLIGLLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQXKXWVGRC 70

Qy 85 HCYFYSMEKKDWNSSLKFCADKGSLLHTFPDQGVKLFGEYLGQDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNSRHLCASQKSLQLQNTDDELDFMSS--SQQFYWIGLSYSEHTAW 128

Qy 142 RWEGGPALSRLITN---SLIQRCGAHRNG-LQASSCEVALQWICKKVL 187
Db 129 LWENGSAISOYLFPSPFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 10
US-09-113-789-9
; Sequence 9, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
```

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
; US-09-113-789-9

Query Match 17.3%; Score 178.5; DB 3; Length 179;
Best Local Similarity 31.8%; Pred. No. 3.5e-12;
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLLTVILMSLLMYQRIILCCGS-----KSTCSHCPCSPILWTRNGS 84
Db 14 GTLGIIICLSMATLIGLLKNSFTKLSIEPAFTPGPNIELQKSDC--C-SCQXKXWVGRC 70

Qy 85 HCYFYSMEKKDWNSSLKFCADKGSLLHTFPDQGVKLFGEYLGQDFYWGIRNID---GW 141
Db 71 NCYFISSEQKTWNSRHLCASQKSLQLQNTDDELDFMSS--SQQFYWIGLSYSEHTAW 128

Qy 142 RWEGGPALSRLITN---SLIQRCGAHRNG-LQASSCEVALQWICKKVL 187
Db 129 LWENGSAISOYLFPSPFTNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178

RESULT 11
PCT-US93-10418-2
; Sequence 2, Application PC/TUS9310418
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Hjerild, Kathryn A.
; TITLE OF INVENTION: Activation Antigen CD69
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10418
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2610-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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```
RESULT 14
PCT-US94-07587-2
; Sequence 2, Application PC/TUS9407587
; GENERAL INFORMATION:
; APPLICANT: Schering Corp.
; TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
; TITLE OF INVENTION: RELATED REAGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering Corp.
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07587
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lund, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: DX0397K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7255
; TELEFAX: 201-822-7039
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07587-2

Query Match 16.0%; Score 164.5; DB 5; Length 225;
Best Local Similarity 27.4%; Pred. No. 1.8e-10;
Matches 60; Conservative 32; Mismatches 90; Indels 37; Gaps 10;

Qy 1 MADSIYSTLELP--EAPQ-----VDSRWKLVKAVLHRLPHLSRFAMVALGL--- 45
Db 1 MDQQAIVAEINLPTDGPSESSPSLPDVCQGPSWHQFAL----KLSGAGIILLVLVVT 56
Qy 46 -LTVILMSLLMYQRIILCG-----SKDSTCSH--CPSCPILWTRNGSHCYFYSMEKKDWN 97
Db 57 GLSVSVISLIQKSKIEKCSVDIQSRNKTTPRGILNCPYVQQQLREKCLLFSTVNPWN 116
Qy 98 SSLKFCADRGSHLLTFPDNQGVKLFGBYLQD---FYWIGLR---NIDGWRWEGGPALS- 150
Db 117 NSLADCSKTKESSLILIRDKDEL-IHTQNLIRDKAILEWIGLNFSLSEKNKWKINGSFLNS 175
Qy 151 --LRILTNSLIQRCGAHRNGLQASSCEVALQWICKVL 187
Db 176 NDLEIRGDAKENSICISISQTSVYSEYCSYCTEIRWICQKEL 214

RESULT 15
US-09-531-056A-6
; Sequence 6, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 6
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-6

Query Match 15.9%; Score 163.5; DB 4; Length 191;
Best Local Similarity 25.3%; Pred. No. 1.9e-10;
Matches 50; Conservative 21; Mismatches 78; Indels 49; Gaps 7;

Qy 11 ELPEAPQVQDESRLKLVKAVLHRLPHLSRFAMVALGLLTVI--LMSLLMYQRIILCG----- 63
Db 15 ELPANPGLSHKHSIKA-----TLIWLRLFLINFLTIIVCGMVAAL 56
Qy 64 -SKDSTCSHCP-----CPILWTRNGSHCYFYSMEKKDWNSSILKFCADRGSHLLTFPDN 116
Db 57 SAIRANCHQEPSPVCLQAACPESWIGFQKCYFSDDTKNWTSSQRFCDSDADLAQVESF 116
Qy 117 QGVKLFGEYLGQDFYWIGLGNIDG--WRWEGG-----PALSRLITLNSLIQRCGAHR 167
Db 117 QELNELLRYKGPSDHWIGLSREOGQPKWKWINGTEWTRQFFILG-----AGECAYLND 168
Qy 168 NGLQASSCEVALQWICKK 185
Db 169 KGASSARHYTERKWICKK 186

Search completed: August 10, 2004, 16:20:31
Job time : 14.6407 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 11.9788 Seconds
(without alignments)
1509.673 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAPRVQD.....GLHASCEVALQWICEKVLVLP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Piri:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2 I59421	mast cell function
2	184.5	17.8	199	2 JH0822	lymphocyte early a
3	184	17.8	257	2 I50146	gene 17.5 protein
4	172.5	16.7	227	2 A46467	natural killer cell
5	169.5	16.4	225	2 I38700	hNKR-P1a protein
6	167	16.1	223	2 B46467	NKR-P1 protein hom
7	165.5	16.0	301	1 LNRT2	hepatic lectin 2 -
8	162.5	15.7	170	2 T28140	natural killer cell
9	159.5	15.4	220	2 C46467	NKR-P1 protein hom
10	159.5	15.4	223	2 A35917	NK-cell receptor P
11	159.5	15.4	301	2 S13165	asialoglycoprotein
12	158	15.3	156	2 T28141	C type lectin, B1
13	158	15.3	1487	2 S48719	phospholipase-A(2)
14	157	15.2	216	2 P70375	natural killer cell
15	156	15.1	284	2 S29855	asialoglycoprotein
16	154.5	14.9	304	2 JX0209	lectin, galactose/
17	153.5	14.8	404	2 A46274	HIV gp120-binding
18	153.5	14.8	742	2 J75595	scavenger receptor
19	148.5	14.3	306	2 A42230	lycetin M-ASGP-BP p
20	148	14.3	237	2 J7608	type II lectin-like
21	146	14.1	143	2 J71135	agglutinin beta
22	142.5	13.8	236	2 P70372	natural killer cell
23	142.5	13.8	359	2 A43532	B-cell surface ant
24	141.5	13.7	1326	2 A36395	secretory phosphol
25	141.5	13.7	1465	2 A56395	secretory phosphol
26	140.5	13.6	311	1 LNHR2A	asialoglycoprotein
27	139	13.4	240	2 I54524	natural killer cell
28	139	13.4	284	1 LNRTL	hepatic lectin - r
29	137	13.2	167	1 WNVZF2	hepatic lectin hom

hepatic lectin - c
natural killer cel
agglutinin alpha cha
mannose receptor,
hepatic lectin H1
versican precursor
phospholipase A2 r
IgE Fc receptor, l
Kupffer cell recep
versican precursor
versican precursor
ly-49G.2 antigen -
versican precursor
IgE Fc receptor II
coagulation factor
receptor DEC-205 -

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59421
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A:Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C:Genetics:
A:Gene: mafa

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.2e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MADNSIYSTLELPAPRVQDSSRWKAVLRPCVSYLVWVAGLLTVILMSLLLYORTL	60
Db	1	MADNSIYSTLELPAPRVQDSSRWKAVLRPCVSYLVWVAGLLTVILMSLLLYORTL	60
Qy	61	CCGSKGFMCCQCSRCPNLWRNGSHCYFFSMKRDWNSSLKFCADKSGSHLLTFPDNQGVN	120
Db	61	CCGSKGFMCCQCSRCPNLWRNGSHCYFFSMKRDWNSSLKFCADKSGSHLLTFPDNQGVN	120
Qy	121	LFQYVGEDFYWIGLRIDGWRWEDGPAISLSILNSVQKCGTHRCGLHASCEVALQ	180
Db	121	LFQYVGEDFYWIGLRIDGWRWEDGPAISLSILNSVQKCGTHRCGLHASCEVALQ	180
Qy	181	WICEKVLP 188	
Db	181	WICEKVLP 188	

RESULT 2

JH0822
lymphocyte early activation antigen AIM/CD69 - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Oct-1999
C:Accession: JH0822; I56167; S60753
R:Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M
J. Exp. Med. 178, 537-547, 1993
A:Title: Molecular cloning, expression, and chromosomal localization of the human earli
mitting receptors.
A:Reference number: JH0822; MUID:93340630; PMID:8340758
A:Accession: JH0822
A:Molecule type: mRNA

A:Residues: 1-199 <LOR>
A:Cross-references: GB:Z22576; NID:G397938; PIDN:CAA80298.1; PID:G397939
A:Note: the authors translated the codon CAA for residue 110 as GLU
R:Hamann, J.; Fiebig, H.; Strauss, M.
J. Immunol. 150, 4920-4927, 1993
A:Title: Expression cloning of the early activation antigen CD69, a type II integral membrane protein
A:Reference number: I56167; MUID:93267093; PMID:8496594
A:Accession: I56167
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-199 <RES>
A:Cross-references: GB:L07055; NID:G291897; PIDN:AAB46359.1; PID:G291898
R:Sanitis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
Eur. J. Immunol. 24, 1692-1697, 1994
A:Title: Structure of the gene coding for the human early lymphocyte activation antigen receptors.
A:Reference number: S60753; MUID:94298875; PMID:8026529
A:Accession: S60753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <SAN>
A:Cross-references: EMBL:Z30426; NID:G525242; PIDN:CAA83017.1; PID:G558352
C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in C-Genetics:
A:Gene: GDB:CD69
A:Cross-references: GDB:132925; OMIM:107273
A:Map position: 12p13-12p12
C:Superfamily: C-type lectin homology
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:39-64/Domain: transmembrane #status predicted <TM>
F:85-194/Domain: C-type lectin homology <LCH>
F:18,30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 17.8%; Score 184.5; DB 2; Length 199;
Best Local Similarity 26.3%; Pred. No. 4.7e-10;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
QY 35 VSYLVVVALGLLTIVMSLLLYORTLCCSGKGMCSQSRCPNLWMRNGSHCYFYSME 91
DB 45 VNVVFIILLIALISVGQVN---CQGYTFSPSHVSSCSSEDWVGQYQKCYFIST 101
QY 92 EKRDWNSLKFCAADKSHLLTTPDNGQVNLFOYVGEDFYWIGLRDIDG---WRWEDGPAL 149
DB 102 VKRSWTSQACNACSEHGATLAVIDSEKDMFLKRYAGREHWGLKKEPCHPWKNGKSEF 161
QY 150 SLISLSNSVQKCGTHRCGLHASSCEVALQWICEK 185
DB 162 N-WNFVNTGSDKCVFLKNTVSSMECEKNLYWICNK 196
RESULT 3
I50146
gene 17.5 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50146
R:Bernot, A.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 221-229, 1994
A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
A:Reference number: I50146; MUID:94164691; PMID:8119728
A:Accession: I50146
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-257 <BER>
A:Cross-references: GB:M88072; NID:G505324; PIDN:AAA48558.1; PID:G505325
C:Superfamily: C-type lectin homology
F:129-241/Domain: C-type lectin homology <LCH>
Query Match 17.8%; Score 184; DB 2; Length 257;
Best Local Similarity 28.6%; Pred. No. 6.8e-10;
Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

QY 33 PCVSYLVVVALGLLTIVMSLLLYORTLCCSGKGMCSQSRCPNLWMRNGSHCYFYSME 92
DB 101 PC-----MLVLAVAVIL-----ORPSCSPRPFP-----SHVCPNANWVGQKCYFIST 146
QY 93 KRDWNSLKFCAADKSHLLTTPDNGQVNLFOYVGEDFYWIGLRDIDG---WRWEDGPAL 149
DB 147 ESDWNSRREHCHRLGASLATLDTKEEMEFMLQYQRPADRWIGLHRAEGDEHTWADGSF 206
QY 150 SLISLSNSVQKCGTHRCGLHASSCEVALQWICEK 185
DB 207 T-----NRPFVELRGGRCAYLNGDGISSALCHSEKFWVCGR 243
RESULT 4
A46467
natural killer cell receptor p1 - mouse
N:Alternate names: NKR-P1 protein
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change 05-May-2000
C:Accession: A46467; A46502; A46456
R:Giorda, R.; Trucco, M.
J. Immunol. 147, 1701-1708, 1991
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated killer cells
A:Reference number: A46467; MUID:91349596; PMID:1880421
A:Accession: A46467
A:Molecule type: mRNA
A:Residues: 'MELLCT', 1-227 <GIO>
A:Cross-references: GB:M77676; NID:G200058
A:Experimental source: A-LAK cells, C57BL
A:Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence R:Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.
J. Immunol. 149, 1957-1963, 1992
A:Title: Genomic structure and strain-specific expression of the natural killer cell receptor p1
A:Reference number: A46502; MUID:92388663; PMID:1517565
A:Accession: A46502
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 'H', 111-181, 'D', 183-227 <GI2>
A:Cross-references: GB:X64716; NID:G53395; PIDN:CAA45971.1; PID:G817989
A:Experimental source: BALB/c 3T3 fibroblastoid cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072)
R:Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.
J. Immunol. 147, 3229-3236, 1991
A:Title: cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of NKR-P1
A:Reference number: A46456; MUID:92013158; PMID:1680927
A:Accession: A46456
A:Molecule type: mRNA
A:Residues: 1-38, 'L', 40-227 <YOK>
A:Cross-references: GB:M77753; NID:G198569; PIDN:AAA39366.1; PID:G198570
A:Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C:Superfamily: natural killer cell receptor p1; C-type lectin homology
F:94-210/Domain: C-type lectin homology <LCH>
Query Match 16.7%; Score 172.5; DB 2; Length 227;
Best Local Similarity 24.4%; Pred. No. 7.2e-09;
Matches 53; Conservative 35; Mismatches 86; Indels 43; Gaps 8;
QY 6 IYSTILELPAAAPRVQDDSRWKV-----KAVLHRPCVSYLVVVALGLLTIVMSLL 54
DB 6 VYFGLKPEPTPGAWHESPPSLPPDACPCFRSHALKLSCAGLILV-----VTILGMSVL 61
QY 55 -----LYQRTLCCSGKGMCSQSRCPNLWMRNGSHCYFYSMEKEDWNS 99
DB 62 VRVLIQKPSIEKCVLQENL---NKTTCGAKLECPQDWLSHRDKCFHVQSVNTWEEG 118
QY 100 LKFCADKSHLLTTPDNGQVNLFOYVGEDF--YWIGLR-----DIDGWEDGPALS--- 150
DB 119 LVDCDGGKATMLIQDQELRFLDLSIKEKYNFSWIGLRYTLPDWN--NKWINGSTLNSDV 177
QY 151 LSILNSVQKCGTHRCGLHASSCEVALQWICEKVL 187
DB 178 LKITGDTENDSCAAISGDKVTTFESCSNDRWICQEL 214

```
RESULT 5
I38700
hNKR-P1a protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I38700
R;Janier, L.L.; Chang, C.; Phillips, J.H.
J. Immunol. 153, 2417-2428, 1994
A;Title: Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin superfamily ex
A;Reference number: I38700; MUID:94358407; PMID:8077657
A;Accession: I38700
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-225 <RES>
A;Cross-references: EMBL:U11276; NID:g538270; PIDN:AAA21605.1; PID:g544496
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 16.4%; Score 169.5; DB 2; Length 225;
Best Local Similarity 26.1%; Pred. No. 1.4e-08;
Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;

QY 1 MADNSIYSTLELP-----AAPR-VQDDSRKVKAVLHRC--VSYLVMVALGLL 46
Db 1 MDQQAIVAEMLPDTSGPSSPSLPRDVCQGSFWH-QFALKUSCAGIILLVLVVTG-L 58
QY 47 TVILMSLLLYQRTLCGSGKGMFCQCS-----SIEKSVDIQSRNKTTERPGLNCPYQQLREKCLLF 89
Db 59 SVSVTSLI-QKS-----SIEKSVDIQSRNKTTERPGLNCPYQQLREKCLLF 108
QY 90 SMEKRDVNSLKFADKGGSHLLTFPDQGVNLFQYVGED--FWIGLR----DIDGWRWE 144
Db 109 SHTVNPWNLSADGSTRESSLLIRDKDELHTQNLIRDKAILFHWIGLNFSLSEKNKWI 168
QY 145 DGPALS---ILSNSVVQKGTTHRCGLHASSCEVALQWICEKVL 187
Db 169 NGSFLNSNDLEIRGDAKENSICISQTSVSYSEYCSTEIRWICQKEL 214

RESULT 6
B46467
NKR-P1 protein homolog - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C;Accession: B46467
R;Giorda, R.; Trucco, M.
J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill
A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: B46467
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223 <GIO>
A;Cross-references: GB:M77677; NID:g200060; PIDN:AAA39823.1; PID:g200061
A;Experimental source: NK cells, C57BL/7B
A;Note: sequence extracted from NCBI backbone (NCBIN:52380, NCBI:P:52381)
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: transmembrane protein
F;94-210/Domain: C-type lectin homology <LCH>

Query Match 16.1%; Score 167; DB 2; Length 223;
Best Local Similarity 23.3%; Pred. No. 2.3e-08;
Matches 50; Conservative 34; Mismatches 91; Indels 40; Gaps 8;

QY 6 IYSTLELPAARVQDSD-----RKVKAVLHRCPCVSY-----LVVMVALGLL 46
Db 7 VYADINLARIQEPKHDSPPSLSPDTCRCPRW-----HRLALKFCAGIILLVLVVIHLC 60
QY 47 TVILMSLLLYQRTLCG-----SKGFMCSQCSRCPNLWRNMGSHCYFYSMEKRDVNSLSLK 101
Db 61 VLVLVSQKSSVQKICADVQENRTHITDCSVNLCECPQDLNLSHRDKCFRVFQVSNTWEEGQA 120
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```
QY 102 FCADKGGSHLLTFPDQGVNLFQYVGEDF--VWIGLR----DIDGWRWEDGPALS---LS 152
Db 121 DCGRGATLLLIQDBELRLLDSIKKYNFVIGLRFUPLDMN-MKWINGTTFNSVLK 179
QY 153 ILSNSVVQKGTTHRCGLHASSCEVALQWICEKVL 187
Db 180 ITGDTENGSCASISGDKVTSESCTDNRWICQKEL 214

RESULT 7
LNRT2
hepatic lectin 2 - rat
N;Alternate names: asialoglycoprotein receptor RHL-2/3 (ASGP-R2/3)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1988 #sequence_revision 09-Apr-1998 #text_change 22-Jun-1999
C;Accession: B28462; A28462; A31601; A26888; A25417
R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J.
J. Biol. Chem. 262, 9828-9838, 1987
A;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are indepen
A;Reference number: A28462; MUID:87250656; PMID:3597443
A;Accession: B28462
A;Molecule type: mRNA
A;Residues: 1-301 <HAL>
A;Cross-references: GB:J02762; NID:g205162; PIDN:AAA41522.1; PID:g205163
A;Accession: A28462
A;Molecule type: protein
A;Residues: 88-96; 'X', 98-118, 'X', 120-129-158; 177-182, 'X', 184, 'X', 186-189; 192-290, 'C', 29
R;Sanford, J.P.; Elliott, R.W.; Doyle, D.
DNA 7, 721-728, 1988
A;Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.
A;Reference number: A31601; MUID:89170119; PMID:3234178
A;Accession: A31601
A;Molecule type: mRNA
A;Residues: 1-301 <SAN>
A;Cross-references: GB:X07636; NID:g57066; PIDN:CAA30476.1; PID:g57067
R;McPhaul, M.; Berg, P.
Mol. Cell. Biol. 7, 1841-1847, 1987
A;Title: Identification and characterization of cDNA clones encoding two homologous pro
A;Reference number: A26888; MUID:87257885; PMID:3600647
A;Accession: A26888
A;Molecule type: mRNA
A;Residues: 1-152, 'A', 154-201, 'I', 203-259, 'C', 261-301 <MCP>
A;Cross-references: GB:M16347; NID:g206648; PIDN:AAA42038.1; PID:g206649
A;Note: the authors translated the codon GCA for residue 153 as Arg and ATT for residue
R;Drickamer, K.; Mamou, J.F.; Binns, G.; Leung, J.O.
J. Biol. Chem. 259, 770-778, 1984
A;Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evi
A;Reference number: A25417; MUID:84111554; PMID:6319386
A;Accession: A25417
A;Molecule type: protein
A;Residues: 201-259, 'C', 261-281, 'ND', 284-301 <DRI>
C;Comment: Calcium is required for ligand binding.
C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: endocytosis; glycoprotein; lectin; liver; receptor; transmembrane protein
F;2-60/Domain: intracellular #status predicted <IN>
F;61-77/Domain: transmembrane #status predicted <TRN>
F;78-301/Domain: extracellular #status predicted <EXT>
F;170-293/Domain: C-type lectin homology <LCH>
F;97,119,165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.0%; Score 165.5; DB 1; Length 301;
Best Local Similarity 27.3%; Pred. No. 4.4e-08;
Matches 39; Conservative 22; Mismatches 67; Indels 15; Gaps 3;

QY 58 RFLCCGSGFMCSQCSRCPNLWRNMGSHCYFYSMEKRDVNSLSLKFCADKGGSHLLTFPDNQ 117
Db 153 RFLFCQLAFFLSNGTECCPVNWFVGSGCYFWSRDGLTWAEADQYCCQWENAHLLVINSRE 212
QY 118 GVNLFQYVGEDFWIGLRIDG-WRWEDEGPALESLSLSNSVQ-----KCG 163
Db 213 EQEFVWKRGAFTWIGLTDKSGWKVVDGTEYRSFNKNAFTQPDNQQHEGGSDECA 272
```

QY 164 THRCGL-HASCEVALOWICEK 185
 Db 273 EILSDGLWDFNFCQVNRWACER 295

RESULT 8
 T28140
 natural killer cell receptor homolog - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T28140
 R:Milne, S.; Kaufman, J.; Beck, S.
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility complex
 A:Reference number: Z20475
 A:Accession: T28140
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-170 <MIL>
 A:Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
 A:Experimental source: clone cB12
 C:Genetics:
 A:Gene: B-NK
 A:Map position: 16
 A>Note: Intron positions not resolved (incomplete sequence)

Query Match 15.7%; Score 162.5; DB 2; Length 170;
 Best Local Similarity 28.1%; Pred. No. 4.8e-08;
 Matches 34; Conservative 16; Mismatches 60; Indels 11; Gaps 3;

QY 72 CSRCNLWNRNGSHCYFYSMEKRDWNSLKFCADKSGSHLLTPPDNQGNLFQFYVGEDFY 131
 Db 47 CLLCPQFWLLGDRCYELSTEGKNTQAKMKCNLSQSLAVLRKKAEDHLLQMGAGEPV 106

QY 132 WIGLR-DIDGWEDGPALE-----SLSLNSVVKCGTHRCGLHASCEVALOWICEK 184
 Db 107 WIGLRVSTNQMKVDNSNSTESDNLVSMEN---RCGTFKNTKVEGDVCSGEGHWVCQ 162

QY 185 K 185
 Db 163 K 163

RESULT 9
 C46467
 NKRP-1 protein homolog gene-40 - mouse
 N:Alternate names: natural killer cell activation molecule; NK1.1 alloantigen
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
 C:Accession: C46467; A46499
 R:Giorda, R.; Trucco, M.
 J. Immunol. 147, 1701-1708, 1991
 A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated killer cells
 A:Reference number: A46467; MUID:91349596; PMID:1880421
 A:Accession: C46467
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <GIO>
 A:Cross-references: GB:M77678; NID:g200062; PIDN:AAA39824.1; PID:g200063
 A:Experimental source: NK cells, C57BL/7B
 A>Note: Sequence extracted from NCBI backbone (NCBIN:52382, NCBI:P:52383)
 R:Ryan, J.C.; Turck, J.; Niemi, E.C.; Yokoyama, W.M.; Seaman, W.E.
 J. Immunol. 149, 1631-1635, 1992
 A:Title: Molecular cloning of the NK1.1 antigen, a member of the NKRP-1 family of natural killer cell receptors
 A:Reference number: A46499; MUID:92373004; PMID:1506685
 A:Accession: A46499
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-86, 90-220 <RYA>
 A:Cross-references: GB:S43141; NID:g254094; PIDN:AA222979.1; PID:g254095
 A:Experimental source: C57BL/6J NK cells
 A>Note: Sequence extracted from NCBI backbone (NCBIN:111622, NCBI:P:111624)
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology

C:Keywords: transmembrane protein
 F:91-207/Domain: C-type lectin homology <LCH>

Query Match 15.4%; Score 159.5; DB 2; Length 220;
 Best Local Similarity 25.3%; Pred. No. 1.2e-07;
 Matches 46; Conservative 33; Mismatches 74; Indels 29; Gaps 8;

QY 27 KAVLHRPCVSLVMVALGLLTVILMSLLY-----QRTLCGSKGFCMCSQCSR----- 74
 Db 38 RLALKLSACGLILLV-----LTLIGMSVLVRVLVQKPSREKCC---VFIQENLNKTTVNLE 90

QY 75 CENLWNRNGSHCYFYSMEKRDWNSLKFCADKSGSHLLTPPDNQGNLFQFYVGEDF--YW 132
 Db 91 CFQDMLLRDKCFHVSQVSNWEEGQDCGRKAGATLLIQDEELFLDLSIKEXNSFW 150

QY 133 IGLR-----DIDGWEDGPALESLSLNSVVK-----CGTHRCGLHASCEVALOWICEK 185
 Db 151 IGLRFTLPDMN-WKWINGTTFNSDLKITGVTEGSCASILGDKVTPSCASDNRWICQK 209

QY 186 VL 187
 Db 210 EL 211

RESULT 10

A35917
 NK-cell receptor P1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999
 C:Accession: A35917
 R:Giorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.
 Science 249, 1298-1300, 1990
 A:Title: NKRP-1, a signal transduction molecule on natural killer cells.
 A:Reference number: A35917; MUID:90378305; PMID:2399464
 A:Accession: A35917
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-223 <GIO>
 A:Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
 C:Superfamily: natural killer cell receptor P1; C-type lectin homology
 C:Keywords: transmembrane protein
 F:94-210/Domain: C-type lectin homology <LCH>

Query Match

15.4%; Score 159.5; DB 2; Length 223;
 Best Local Similarity 23.5%; Pred. No. 1.2e-07;
 Matches 39; Conservative 33; Mismatches 73; Indels 21; Gaps 5;

QY 38 LVMVALGLLTVILMS-----LILYQRTLCGSKGFCMCSQCSRCPNLWNRNGSHCYFF 89
 Db 54 LALVGMSTLVRVLVQKPSVEPCRVLIQENLSKTGSPAKL-----KCPKDWLSHRDKCFHV 108

QY 90 SMEKRDWNSLKFCADKSGSHLLTPPDNQGNLFQFYV-----EDFYWIGLR---DIDGWWE 144
 Db 109 SQTSTWKEKSLADCGGKATLLVQDQDEELFLRLNLTKRISSESPFWIGLSTLSDENWKVI 168

QY 145 DGPALS---LSILNSVVKCGTHRCGLHASCEVALOWICEKVL 187
 Db 169 NGSTLNSDVLSTGTEKDSKASVSQDKVLSESCSDSNWVQCQEL 214

RESULT 11

S13165
 asialoglycoprotein receptor - mouse
 N:Alternate names: hepatic lectin
 C:Species: Mus musculus (house mouse)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
 C:Accession: S13165
 R:Sanford, J.P.; Doyle, D.
 Biochim. Biophys. Acta 1087, 259-261, 1990
 A:Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor gene
 A:Reference number: S13165; MUID:91027942; PMID:2223888
 A:Accession: S13165
 A:Molecule type: mRNA

[illegible]

F:153-276/Domain: C-type lectin homology <LCH>

```
Query Match      15.1%; Score 156; DB 2; Length 284;
Best Local Similarity 25.6%; Pred. No. 3.2e-07;
Matches 41; Conservative 20; Mismatches 75; Indels 24; Gaps 4;

QY 52 SLLLYQRTLCGSKGFM-----SQCSRCPNLWRNGSHCYFYSMEKRDWNSILKF 102
   ||||: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SLLLVKQLVSDVRSLSQMAAFRCNGSGERTCCPINWVEYEGSCYWFSSVFPWTEADKY 180
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 103 CADKGSLLTTPDNGVNLFPQYVGEDFYWIGLRDIDG--RWEDGPAISLSILS----- 155
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 COLENAHLVVTTSRDEQNFLORHMGPLNTWIGLTDQNGFPKWVDGTDYETGFQNRPREOP 240
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 156 -NSVVQKCGTIHRCGLHASS-----CEVALQWICEKVL 187
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 DNWYGHGLGGEDCAHFTTDGRWDDVCRRPYRWVCETKL 280
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: August 10, 2004, 16:19:36
Job time : 11.9788 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:41 ; Search time 7.32035 Seconds
(without alignments)
1337.256 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSTLELPAAPRVQD.....GLHASCEVALQWICEKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184.5	17.8	199	1	CD69_HUMAN
2	172.5	16.7	227	1	P27811 mus musculus
3	167	16.1	223	1	NK12_MOUSE
4	163.5	15.8	179	1	Q8mzx9 macaca mula
5	161.5	15.6	301	1	LECI_RAT
6	159.5	15.4	220	1	NK14_MOUSE
7	159.5	15.4	223	1	NK13_RAT
8	159.5	15.4	201	1	LECI_MOUSE
9	159	15.3	216	1	NKGD_MACMU
10	157	15.2	216	1	NKGD_HUMAN
11	155	15.0	179	1	CD94_HUMAN
12	155	15.0	179	1	CD94_PANTR
13	154.5	14.9	304	1	MMGL_MOUSE
14	154	14.9	163	1	V239_FOWPV
15	154	14.9	199	1	CD69_MOUSE
16	154	14.9	283	1	LECH_MOUSE
17	153.5	14.8	149	1	CLE2_HUMAN
18	152	14.7	240	1	NKGE_PANTR
19	149.5	14.4	233	1	NKGA_PANTR
20	148.5	14.3	333	1	RMGA_AGRKH
21	148.5	14.3	306	1	MMGL_RAT
22	143.5	13.9	233	1	NKGA_MACMU
23	142.5	13.8	233	1	NKGA_HUMAN
24	142.5	13.8	359	1	CD72_HUMAN
25	140.5	13.6	148	1	CVXB_CRODU
26	140.5	13.6	233	1	NKGC_PANTR
27	140.5	13.6	311	1	LECI_HUMAN
28	139.5	13.5	1722	1	LY75_HUMAN
29	139	13.4	240	1	NKGE_HUMAN
30	139	13.4	283	1	LECH_RAT
31	137	13.2	167	1	V008_FOWPV
32	136.5	13.2	207	1	LECH_CHICK
33	134.5	13.0	231	1	NKGC_MACMU

34	134	12.9	290	1	LECH_HUMAN
35	134	12.9	548	1	KUCR_MOUSE
36	134	12.9	2738	1	PGCV_RAT
37	134	12.9	3358	1	PGCV_MOUSE
38	133.5	12.9	231	1	NKGC_HUMAN
39	132.5	12.8	117	1	CHBB_CROHO
40	132.5	12.8	1458	1	PA2R_RABIT
41	131	12.6	157	1	MMHA_AKHA
42	131	12.6	331	1	FCE2_MOUSE
43	131	12.6	550	1	KUCR_RAT
44	131	12.6	3381	1	PGCV_BOVIN
45	130	12.5	146	1	MMHB_AKHA

ALIGNMENTS

RESULT 1					
CD69_HUMAN					
ID _CD69_HUMAN	STANDARD;	PRT;	199 AA.		
AC Q07108;					
DT 01-OCT-1994 (Rel. 30, Created)					
DT 01-OCT-1994 (Rel. 30, Last sequence update)					
DT 15-MAR-2004 (Rel. 43, Last annotation update)					
DE Early activation antigen CD69 (Early T-cell activation antigen p60)					
DE (GP32/28) (Ieu-23) (MLR-3) (EAL) (BL-AC/P26) (Activation inducer molecule) (AIM).					
DE GN CB69.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Blood;					
RX MEDLINE=93267093; PubMed=8496594;					
RA Hamann J., Fiebig H., Strauss M.;					
RT "Expression cloning of the early activation antigen CD69, a type II integral membrane protein with a C-type lectin domain.";					
RL J. Immunol. 150:4920-4927(1993).					
RN [2]					
RP SEQUENCE FROM N.A., AND SEQUENCE OF 96-103; 128-146 AND 189-199.					
RC TISSUE=Blood;					
RX MEDLINE=93340630; PubMed=8340758;					
RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,					
ESch F., Sanchez-Mateos P., Sanchez-Madrid F.;					
RT "Molecular cloning, expression, and chromosomal localization of the human earliest lymphocyte activation antigen AIM/CD69, a new member of the C-type animal lectin superfamily of signal-transmitting receptors.";					
RL J. Exp. Med. 178:537-547(1993).					
RN [3]					
RP SEQUENCE FROM N.A.					
RC MEDLINE=93314711; PubMed=8100776;					
RX Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,					
Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,					
Alderson M.R.;					
RT "Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer cell activation antigens.";					
RL Eur. J. Immunol. 23:1643-1648(1993).					
RN [4]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Placenta;					
RX MEDLINE=94298875; PubMed=8026529;					
RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.;					
RT "Structure of the gene coding for the human early lymphocyte activation antigen CD69: a C-type lectin receptor evolutionarily related with the gene families of natural killer cell-specific receptors.";					
RL Eur. J. Immunol. 24:1692-1697(1994).					
RN [5]					
RP SEQUENCE FROM N.A.					

P07306	homo sapien
P70194	mus musculus
Q9erb4	rattus norv
Q62059	mus musculus
P26717	homo sapien
P81509	crotalus ho
P49260	oryctolagus
Q9ygg9	agkistrodon
P20693	mus musculus
P10716	rattus norv
P81282	bos taurus
Q9yi92	agkistrodon

```

RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in lymphocyte proliferation and functions as a
CC signal transmuting receptor in lymphocytes, natural killer (NK)
CC cells, and platelets.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T-cells,
CC B-cells, natural killer cells, neutrophils, eosinophils, epidermal
CC Langerhans cells and platelets.
CC -!- DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein
CC acquired during lymphoid activation.
CC -!- INDUCTION: By antigens, mitogens or activators of PKC on the
CC surface of T and B lymphocytes. By interaction of IL-2 with the
CC p75 IL-2R on the surface of NK cells.
CC -!- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
CC THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD69 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd69.htm".
CC -----
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CC -----
DR EMBL; L07555; AAB46359.1; -.
DR EMBL; Z22576; CAA80298.1; -.
DR EMBL; Z30426; CAA83017.1; -.
DR EMBL; Z30430; CAA83017.1; JOINED.
DR EMBL; Z30427; CAA83017.1; JOINED.
DR EMBL; Z30429; CAA83017.1; JOINED.
DR EMBL; Z30428; CAA83017.1; JOINED.
DR EMBL; BC007037; AAH07037.1; -.
DR PIR; JH0822; JH0822.
DR PDB; 1E87; 18-JUL-03.
DR PDB; 1E81; 18-JUL-03.
DR Genew; HGNC:1694; CD69.
DR MIM; 107273; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004888; F: transmembrane receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
KW Phosphorylation; 3D-structure.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

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FT DOMAIN 62 199 (POTENTIAL).
FT DOMAIN 92 195 EXTRACELLULAR (POTENTIAL).
FT DISULFID 68 85 C-TYPE LECTIN.
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 199 AA; 22559 MW; 172E2699D2FBBDFB CRC64;

Query Match 17.8%; Score 184.5; DB 1; Length 199;
Best Local Similarity 26.3%; Pred. No. 4.5e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVVVALGHTLVILMSLLLYQRTLCGSKGEMC---SQGSRCPNLMWRNGSHCYFESM 91
DB 45 VNVVVFITILIALSVGGYN---CPGQYTFSPSHVSSCEDWVGQKCYFIST 101
QY 92 EKRDWNSLKFCADKAGKSHLLTFPNQGVNLPQEVYGVDFYWIGLRDIDG--WRWEDGPA 149
DB 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKKEPHEWKSNGKEF 161
QY 150 SLSILSNSVVKCGTTHRCGLHASSCEVALOWICEK 185
DB 162 N-NMFNVTGDKCVFLKNTVSSMECEKNLYWICNK 196

RESULT 2
NK11 MOUSE
ID NK11_MOUSE STANDARD; PRT; 227 AA.
AC P27811;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein P1-2 (NKR-P1 2) (NKR-P1.7).
GN KLRB1A OR LY55A OR LY55.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giorda R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013158; PubMed=1680927;
RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,
RA Seaman W.E.;
RT "cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49.
RT Identification of a natural killer cell gene complex on mouse
RT chromosome 6.";
RL J. Immunol. 147:3229-3236(1991).
CC -!- FUNCTION: May function as signal-transmitting receptor.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; M7676; AAA39822.1; -.
DR EMBL; M7753; AAA39366.1; -.
DR PIR; A46457; A46457.
DR HSPF; P22897; 1EGG.

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SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20322487; PubMed=10866118;
 RA LaBonte M.L., Levy D.B., Letvin N.L.;
 RT "Characterization of rhesus monkey CD94/NGK2 family members and
 RT identification of novel transmembrane-deleted forms of NK2-A, B, C,
 RT and D";
 RL Immunogenetics 51:496-499 (2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21158386; PubMed=11261935;
 RA Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
 RT "Selective expression of NK2-A and NK2-C mRNAs and novel alternative
 RT splicing of 5' exons in rhesus monkey decidua";
 RL Immunogenetics 53:69-73 (2001).
 CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
 CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
 CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NK2G family
 CC members.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=CD94-A;
 CC IsoId=Q9MK9-1; Sequence=Displayed;
 CC Name=2; Synonyms=CD94-B;
 CC IsoId=Q9MK9-2; Sequence=VSP_003055;
 CC Name=3; Synonyms=CD94 alt;
 CC IsoId=Q9MK9-3; Sequence=VSP_003054;
 CC -!- TISSUE SPECIFICITY: Natural killer cells.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC
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 CC
 CC EMBL; AF190931; AAF74527.1; -
 CC EMBL; AF190932; AAF74528.1; -
 CC EMBL; AF190933; AAF74529.1; -
 CC EMBL; AF294886; AAG34498.1; -
 CC HSSP; P22897; 1EGG.
 CC InterPro; IPR001304; Lectin C.
 CC Pfam; PF00059; lectin.c; 1.
 CC SMART; SM00034; CLECT_1.
 CC PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 CC PROSITE; PS50441; C-TYPE LECTIN_2; 1.
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
 KW Alternative splicing; Polymorphism.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT FT
 FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 89 174 BY SIMILARITY.
 FT DISULFID 152 166 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 34 MAVFKTLWRLISGTIGICLSMATLGLKNS -> MAA
 FT FT
 FT VARSPLIC 105 105 /FTID=VSP_003054.
 FT FT
 FT VARIANT 139 139 L -> LQ (in isoform 2).
 FT FT
 FT VARSPLIC 139 139 Y -> D.
 FT FT
 FT SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;
 Query Match 15.8%; Score 163.5; DB 1; Length 179;
 Best Local Similarity 31.2%; Pred. No. 4.7e-09;
 Matches 39; Conservative 19; Mismatches 58; Indels 9; Gaps 4;
 QY 70 SQCSKCPNLWRNGSHCHYFSEKRDWNSSLKFCADKGSLLHTFPDNGQVNLFBQBYVGED 129

Db 56 SDCCSCHEKVGVCNCFISSEKRWESRHFCAQSQSSLLQLQNRDELDFMSS--SQH 113
 QY 130 FWIGL---RDIDGWRWDGPPALSILSNSVVK---CGTHRCG-LHASCEVALQWI 182
 Db 114 FYWIGLSSEHTAWLWENGSAISOYLFPSFTFRKPCNGIAYNSKGNALDESCETKNRYI 173
 QY 183 CEKVL 187
 Db 174 CKQQL 178
 RESULT 5
 LECTIN RAT
 ID LECTIN RAT STANDARD; PRT; 301 AA.
 AC P08290;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Asialoglycoprotein receptor R2/3 (Hepatic lectin 2/3) (RHL-2) (ASGP-R)
 DE (ASGP-R)
 GN ASGR2 OR ASGR-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87257885; PubMed=3600647;
 RA MCPHaul M., Berg P.;
 RT "Identification and characterization of cDNA clones encoding two
 RT homologous proteins that are part of the asialoglycoprotein
 RT receptor";
 RL Mol. Cell. Biol. 7:1841-1847 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250656; PubMed=3597443;
 RA Halberg D.F., Wager R.E., Farrell D.C., Hildreth J., Quesenberry M.S.,
 RA Loeb J.A., Holland E.C., Drickamer K.;
 RT "Major and minor forms of the rat liver asialoglycoprotein receptor
 RT are independent galactose-binding proteins. Primary structure and
 RT glycosylation heterogeneity of minor receptor forms";
 RL J. Biol. Chem. 262:9828-9838 (1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=89170119; PubMed=3234178;
 RA Sanford J.P., Elliott R.W., Doyle D.;
 RT "Asialoglycoprotein receptor genes are linked on chromosome 11 in the
 RT mouse";
 RL DNA 7:721-728 (1988).
 RN [4]
 RP SEQUENCE OF 201-301.
 RX MEDLINE=84111554; PubMed=6319386;
 RA Drickamer K., Mamon J.F., Binns G., Leung J.O.;
 RT "Primary structure of the rat liver asialoglycoprotein receptor.
 RT Structural evidence for multiple polypeptide species";
 RL J. Biol. Chem. 259:770-778 (1984).
 CC -!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to
 CC which the terminal sialic acid residue on their complex
 CC carbohydrate moieties has been removed. The receptor recognizes
 CC terminal galactose and N-acetylgalactosamine units. After ligand
 CC binding to the receptor, the resulting complex is internalized and
 CC transported to a sorting organelle, where receptor and ligand are
 CC disassociated. The receptor then returns to the cell membrane
 CC surface.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
 CC cells.
 CC -!- MISCELLANEOUS: Calcium is required for ligand binding.
 CC -!- MISCELLANEOUS: Two types of rat hepatic lectin have been
 CC identified, RHL-1 and RHL-2/3, having a relative abundance of 4:1.
 CC RHL-2 and RHL-3 only differs in their carbohydrate structures.

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CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; M16347; AAA42038.1; -.
CC EMBL; J02762; AAA41522.1; -.
CC EMBL; X07636; CAA30476.1; -.
CC PIR; B28462; LNR12.
CC HSPSP; P06734; IHLI.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; lectin C.
CC InterPro; IPR005640; lectin_N.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF03954; lectin_N; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
CC Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
CC Calcium; Signal-anchor; Phosphorylation.
KW CAELIUM; SIGNAL-ANCHOR; PHOSPHORYLATION.
FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT SIGNAL-ANCHOR (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT C-TYPE LECTIN (LONG FORM).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .).
FT N-LINKED (GLCNAC. . .).
FT N-LINKED (GLCNAC. . .).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .).
FT CARBOHYD 153 153 R -> A (IN REF. 1).
FT CONFLICT 202 202 I -> N (IN REF. 2 AND 3).
FT CONFLICT 260 260 C -> W (IN REF. 2 AND 3).
FT CONFLICT 260 260 C -> W (IN REF. 2 AND 3).
SQ SEQUENCE 301 AA; 34943 MW; 3C2315E642D71279 CRC64;

Query Match 15.6%; Score 161.5; DB 1; Length 301;
Best Local Similarity 27.3%; Pred. No. 1.3e-08;
Matches 39; Conservative 22; Mismatches 67; Indels 15; Gaps 3;

Qy 58 RTLCGSKGCMSCQSRCPNLWMRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFFPDNQ 117
Db 153 RTLCQAFSLNSGTECCPVNWFVGGSCYWFSDGLTWAEDQYCWMEIAHLVINSRE 212
Qy 118 GVNLFQYVVGEDFWIGLRIDIG-WRWDGDPALSLSLNSVVG-----KCG 163
Db 213 EQEFVWKRGAFAHWIGLTDKSGWKVGDGTEYSNFKNWAFTPDNCQHGEGGEDCA 272
Qy 164 TIHRCGL-HASSCHEVALQWICEK 185
Db 273 EILSDGLWNNDFCQQVNRWACER 295

RESULT 6
NK14_MOUSE
AC P27814; STANDARD; PRT; 220 AA.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Natural killer cell surface protein P1-40 (NKR-P1 40) (NKR-P1.9).
GN KLRLC1 OR LY55-C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
EN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=91349596; PubMed=1880421;
RA Giorda R., Trucco M.;
RT "Mouse NKR-P1. A family of genes selectively coexpressed in adherent
RT lymphokine-activated killer cells.";
RL J. Immunol. 147:1701-1708(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=92373004; PubMed=1506685;
RA Ryan J.C., Turck J., Niemi E.C., Yokoyama W.M., Seaman W.E.;
RT "Molecular cloning of the NK1.1 antigen, a member of the NKR-P1
RT family of natural killer cell activation molecules.";
RL J. Immunol. 149:1631-1635(1992).
CC -I- FUNCTION: May function as signal-transmitting receptor.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein.
CC -I- TISSUE SPECIFICITY: Natural killer cells.
CC -I- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; M77678; AAA39824.1; -.
CC PIR; C46467; C46467.
CC SWISS-2DPAGE; P27814; MOUSE.
CC MGD; MGI:107538; Klrb1c.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; lectin C.
CC Pfam; PF00059; lectin_c; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 63 220 EXTRACELLULAR (POTENTIAL).
FT DISULFID 91 102 C-TYPE LECTIN (LONG FORM).
FT DISULFID 119 207 BY SIMILARITY.
FT DISULFID 186 199 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 220 AA; 24771 MW; 8A160B1DED46398F CRC64;

Query Match 15.4%; Score 159.5; DB 1; Length 220;
Best Local Similarity 25.3%; Pred. No. 1.5e-08;
Matches 46; Conservative 33; Mismatches 74; Indels 29; Gaps 8;

Qy 27 KAVLHRCVSVLYNVALGLTLVILMSLLY-----QRTLCGSKGCMSCQSR----- 74
Db 38 RLALKLSGAGLILIV----LTLIGMSVLVRLVQKPSREKCC---VFQENLAKTITVNL 90
Qy 75 CPNLWMRNGSHCYFYSMEKRDWNSSLKFCADKGSLLTFFPDNQGVNLFQYVVGEDF--Y 132
Db 91 CPQDWLHHRDKCFHVSQVSNVWEEGQADCGKRGATLLIQDBELRFLDSIKEKYNFW 150
Qy 133 IGLR----DIDGWRWDGDPALSLSLNSVVGK---CGTIHRCGLHASSCHEVALQWICEK 185
Db 151 IGLRFTLPDMN-WKWINGTTFNSDLVLTGVTENGSCASILGDKVTFESCADNRWICQK 209
Qy 186 VL 187
Db 210 EL 211

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RESULT 7
ID NK13 RAT STANDARD; PRT; 223 AA.
AC P27471.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cell surface protein PI-3.2.3 (NKR-PI 3.2.3) (Antigen
DE 3.2.3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90378305; PubMed=2399454;
RA Giordano R., Rudert W.A., Vavassori C., Chambers W.H.,
RA Hiserodt J.C., Trucco M.;
RT "NKR-PI, a signal transduction molecule on natural killer cells.";
RL Science 249:1298-1300(1990).
CC -!- FUNCTION: Mediates transmembrane signaling in natural killer
CC (NK) cells and so may act as a receptor able to selectively
CC trigger NK cell activity.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- MISCELLANEOUS: Ligand binding may be calcium dependent.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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QY 145 DGPALSD---LSILNSVQKCGTTHRCGLHASSCEVALQWICBKVL 187
DB 169 NGSTLNSVLSITGTCKDSCASVQDKVLSECSQSDNIWVQCKEL 214

RESULT 8
ID LECI MOUSE STANDARD; PRT; 301 AA.
AC P24721.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)
DE (ASGPR).
DE ASGPR2 OR ASGR-2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91027942; PubMed=2223888;
RA Sanford J.P., Doyle D.;
RA "Mouse asialoglycoprotein receptor cDNA sequence: conservation of
RT receptor genes during mammalian evolution.";
RL Biochim. Biophys. Acta 1087:259-261(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Mediates the endocytosis of plasma glycoproteins to
CC which the terminal sialic acid residue on their complex
CC carbohydrate moieties has been removed. The receptor recognizes
CC terminal galactose and N-acetylgalactosamine units. After ligand
CC binding to the receptor, the resulting complex is internalized and
CC transported to a sorting organelle, where receptor and ligand are
CC disassociated. The receptor then returns to the cell membrane
CC surface.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal
CC cells.
CC -!- MISCELLANEOUS: Calcium is required for ligand binding.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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```


[3] SEQUENCE FROM N.A. (ISOFORM 2).
 RA Blassoni R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 [4] SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=98267245; PubMed=9601951;
 RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
 RA Tokuma S., Inoue T., Yamamoto K., Juji T.;
 RT "A alternatively spliced form of the human CD94 gene";
 RL Immunogenetics 48:87-88(1998).
 [5] SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Blood;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
 class I HLA-E molecules by NK cells and some cytotoxic T-cells.
 CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
 members.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=3;
 Name=1; Synonyms=CD94-A;
 IsoId=Q13241-1; Sequence=VSP_003053;
 Name=2; Synonyms=CD94-B;
 IsoId=Q13241-2; Sequence=VSP_003053;
 Name=3; Synonyms=CD94 alt;
 IsoId=Q13241-3; Sequence=VSP_003052;
 -!- TISSUE SPECIFICITY: Natural killer cells.
 -!- SIMILARITY: Contains 1 C-type lectin family domain.
 -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".

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 EMBL; U30610; AAC50291.1; -;
 EMBL; Y14287; CAA74663.1; -;
 EMBL; Y14288; CAA74663.1; JOINED.
 EMBL; AJ000673; CAA04230.1; -;
 EMBL; AJ000001; CAA03845.1; -;
 EMBL; AB009597; BAA24450.1; -;
 EMBL; AB010084; BAA24451.1; -;
 EMBL; BC028009; AAB28009.1; -;
 PDB; 1B6E; 15-JUN-99.
 EMBL; HGNC:6378; KLRD1.
 MIM; 602894; -;
 GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR GO; GO:0005960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
 KW Alternative splicing; 3D-structure.
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 89 174 BY SIMILARITY.
 FT DISULFID 152 166 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 34 MAYFKTLWRLISGTIGTICLSLMTATIGLLKNS -> MAA
 (in isoform 3).
 FT VARSPLIC 105 105 /FTId=VSP_003052.
 FT L -> IQ (in isoform 2).
 FT /FTId=VSP_003053.
 SQ SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
 Query Match 15.0%; Score 155; DB 1; Length 179;
 Best Local Similarity 27.0%; Pred. No. 3.2e-08;
 Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;
 QY 24 WK-VKAVLHRCPCVSYLVMMVALGILLTVLMSLLLYQRTLCGSKGFM--CSQCSRCPNLWM 80
 DB 9 WRUIGTGLTICLS--LMATIGILLKNSFTKLSIEPAFTGPNIELQKDDCCSCQEKWV 66
 QY 81 RNSGHCVYFSEMEKRDWNSSLKFCADKSGSHLLTFPDNGVNLFOYVGEFYWGL--RRD 137
 DB 67 GYRCNCYCFISSEQKTWNSRHLCASQSKSLQLQNTDELDFMSS--SQQFYWGLSYSEE 124
 QY 138 IDGWRMEDGPALSLISLSNV---VQKCGTHRCG-LHASSCEVALOWICEKVL 187
 DB 125 HTAWLWNGSALSQYLPSPFETNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
 RESULT 12
 CD94 PANTR ID CD94 PANTR STANDARD; PRT; 179 AA.
 AC Q9MZ41;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
 DE lectin-like receptor subfamily D, member 1).
 GN KLRD1 OR CD94.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20350666; PubMed=10894168;
 RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
 RA Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
 RA Parham P.;
 RT "Rapid evolution of NK cell receptor systems demonstrated by
 RT comparison of chimpanzees and humans.";
 RL Immunity 12:687-698(2000).
 RN [2]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=21623889; PubMed=11751968;
 RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
 RA Cleland S., Guehlein L.A., Uhrberg M., Parham P.;
 RT "Conservation and variation in human and common chimpanzee CD94 and

```

RT NKG2 genes.";
RL J. Immunol. 168:240-252(2002).
CC -!- FUNCTION: plays a role as a receptor for the recognition of MHC
CC class I HLA-B molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
CC members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MZ41-1; Sequence=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MZ41-2; Sequence=VSP 003056;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; AF259054; AAF86964.1; -.
DR HSSP; P22897; 1EGG.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE NEG.
DR Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10
FT TRANSMEM 11 31
FT SIGNAL-ANCHOR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 179
FT TRANSMEM 33 179
FT EXTRACELLULAR (POTENTIAL).
FT C-TYPE LECTIN (LONG FORM).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT L -> LQ (in isoform 2).
FT /FTid=VSP 003056.
SQ SEQUENCE 179 AA; 20493 MW; 7244D99ED9587E7 CRC64;

Query Match 15.0%; Score 155; DB 1; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.2e-08;
Matches 47; Conservative 28; Mismatches 85; Indels 14; Gaps 7;

Qy 24 WK-KVAVLHRCVSVLVVAVLGLLTIVLMSLLYQRTLCCKSGKFM--CSQCSRCPNLMW 80
Db 9 WRLISGILGICLS--LMATGILKNSFTKLSIEPAFTPGNIELOKSDCCQCKW 66
Qy 81 RNSGHYFYSMEKDWNSLKFCADKGSLLTFFDNGVNLFOEYVGVDFWIGL---RD 137
Db 67 GYRCNCYFISSEQKTNESRHLCSQKSLQLQNTDELDPWSS--SQQFWIGLSYSEE 124
Qy 138 IDGWRWEDGPALSILSNSV---QKGTTHRCG-LHASCCEVALQWICKVL 187
Db 125 HTAWLWENGSAISQYLFPSFETFPKNCIATNPNGNALDESCEDKNRYICKQL 178

RESULT 13
MMGL_MOUSE
ID MMGL_MOUSE STANDARD; PRT; 304 AA.
AC P49300;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Macrophage asialoglycoprotein-binding protein 1 (M-ASGP-BP)

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DE (Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).
GN MGL1 OR MGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeN;
RX MEDLINE=92268032; PubMed=1587794;
RA Sato M., Kawakami K., Osawa T., Toyoshima S.;
RT "Molecular cloning and expression of cDNA encoding a galactose/N-
RT acetylgalactosamine-specific lectin on mouse tumoricidal
RT macrophages."
RL J. Biochem. 111:331-336(1992).
RN [2]
RP SEQUENCE OF 102-120 AND 137-151.
RC STRAIN=C3H/HeN;
RX MEDLINE=89197865; PubMed=3241002;
RA Oda S., Sato M., Toyoshima S., Osawa T.;
RT "Purification and characterization of a lectin-like molecule specific
RT for galactose/N-acetyl-galactosamine from tumoricidal macrophages."
RL J. Biochem. 104:600-605(1988).
CC -!- FUNCTION: Recognizes terminal galactose and N-acetylgalactosamine
CC units. May participate in the interaction between tumoricidal
CC macrophages and tumor cells.
CC -!- SUBUNIT: Homooligomer.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated
CC macrophages.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; S36676; AAB22171.1; -.
DR PIR; JX0209; JX0209.
DR HSSP; P06734; 1HLI.
DR MGD; MGI:96975; Mgl1.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR005640; Lectin_N.
DR Pfam; PF03954; lectin_N; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; Glycoprotein; Transmembrane; Calcium; Signal-anchor.
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT SIGNAL-ANCHOR (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT C-TYPE LECTIN (LONG FORM).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166
FT CARBOHYD 304 AA; 34596 MW; 3F79CD12C34F5BCC CRC64;
SQ SEQUENCE 304 AA; 34596 MW; 3F79CD12C34F5BCC CRC64;

Query Match 14.9%; Score 154.5; DB 1; Length 304;
Best Local Similarity 27.8%; Pred. No. 6.4e-08;
Matches 37; Conservative 19; Mismatches 62; Indels 15; Gaps 3;

Qy 70 SQSRCPNLMWRNGSHCHYYSMEKRDWNSLKFCADKGSLLTFFDNGVNLFOEYVGV 129
Db 168 SEVACCPHLHWTEHSGYWFSEKSWPEADKYCRLENSHLVVVNSLEQNFLORLANV 227

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QY 130 FWVIGLRDIDG-WRWEDGPAISLSILNSVVQ-----KCGTHRCG-LHASS 174
Db 228 VSMIGLTDQNGPWRWYDGTDFEKFGKNWAPLPDNGFCHGLGGEDCAHITTGPNWDDV 287
QY 175 CEVALOWICEKVL 187
Db 288 CQTFRWICBMKL 300

RESULT 14
ID V239_FOWPV STANDARD; PRT; 163 AA.
AC F1437L; Q9J500;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative C-type lectin protein FPV239 (BamHI-ORF8).
GN FPV239.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Alfonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus."
RL J. Virol. 74:3815-3831(2000).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RC STRAIN=FP-9 / Isolate HP-438;
RX MEDLINE=88229622; PubMed=2836548;
RA Tomley F., Birns M., Campbell J., Boursnell M.E.G.;
RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
of fowlpox virus."
RL J. Gen. Virol. 69:1025-1040(1988).
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; AF198100; AAP44583.1; -.
DR EMBL; D00295; BAA0203.1; -.
DR PIR; H29963; WMVZF8.
DR HSSP; P05140; 2AFP.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Hypothetical protein; Lectin.
FT DOMAIN 48 159 C-TYPE LECTIN.
SQ SEQUENCE 163 AA; 18635 MW; 5156DC892885532 CRC64;

Query Match 14.98; Score 154; DB 1; Length 163;
Best Local Similarity 22.94; Pred. No. 3.7e-08;
Matches 38; Conservative 31; Mismatches 65; Indels 32; Gaps 5;

QY 33 PCVSLVWVALGILTVILMS-----LLLYQRTLCGSGFGMCSQSRCPNLMRNGS 84
Db 18 PCGS--IIIVLSFVILSTRPVPDPKILY-----CKEGWGVYKN 57
QY 85 HCYYFSMEKRDWNSSLKFCADKGSLLTFFPDNGVNLFOYVGBDFWIGLRDID---GW 141
Db 58 NCYFFSEKNKNSLAVERCKDMGHLTSISSKEBFKFLRYKPGNHWIGIEKVDENGTV 117
QY 142 RWEDGPAISLSILNSVVQKCGTHRCGLHASSCEVALOWICEKVL 187

Db 118 KLEDSSYD-NIVPIKGIDGCAVLSDRSINMSFCFLPKKWICKIIL 162

RESULT 15
ID CD69_MOUSE STANDARD; PRT; 199 AA.
AC F37217;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Early activation antigen CD69.
GN CD69.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314711; PubMed=8100776;
RA Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
RA Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
RA Alderson M.R.;
RT "Molecular characterization of the early activation antigen CD69: a
type II membrane glycoprotein related to a family of natural killer
cell activation antigens."
RL Eur. J. Immunol. 23:1643-1648(1993).
CC -1- FUNCTION: Involved in lymphocyte proliferation and functions as a
signal transmitting receptor in lymphocytes, natural killer (NK)
cells, and platelets.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS,
B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.
CC -1- DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein
acquired during lymphoid activation.
CC -1- INDUCTION: By the activation of T lymphocytes.
CC -1- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
THYMOCYTES AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; L23638; -. NOT_ANNOTATED_CDS.
DR MGD; MGI:89343; CD69.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein;
Phosphorylation.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 62 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 195 C-TYPE LECTIN.
FT DISULFID 68 85 BY SIMILARITY.
FT DISULFID 96 194 BY SIMILARITY.
FT DISULFID 173 186 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 199 AA; 22517 MW; 39F8E4941D36D4F6 CRC64;
```

Query Match 14.9%; Score 154; DB 1; Length 199;
Best Local Similarity 22.7%; Pred. No. 4.6e-08;
Matches 35; Conservative 32; Mismatches 71; Indels 16; Gaps 4;

Qy	45	LLTVILMSLLLYQRTLCGSKGFC-----SQSRCPNLWMENGSHCHYFSMEK	93
Db	46	LIVVLTSLIITALINVGK--YNPCGLYEKLESSDHHVATCKNEWISYKRTCYFFSTTT	103
Qy	94	RDWNSLKFCAKSGSHLLTFPDNQGVLNFQYVGEDFYWIGLRD--IDGWRWEDGPALS	151
Db	104	KSWALAQRSCEADATLAVIDSEKDMTFLKRYSGLEHWHIGLKNEANQTKWANGKEFN-	162
Qy	152	SILNSVVQKCGTIHRCGLHASSCEVALQWICEK	185
Db	163	SWFNLTGSGRCVSVNHKNVTAVDCEANPHWVCSK	196

Search completed: August 10, 2004, 16:17:00
Job time : 7.32035 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:11:32 ; Search time 32.6089 Seconds
(without alignments)
1819.059 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSLLEPAAPRVQD.....GLHASCEVALQWICEKVL 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	11 Q64335	Q64335 rattus norv
2	838	80.9	188	11 Q88713	Q88713 mus musculu
3	545.5	52.7	189	4 Q75613	Q75613 homo sapien
4	541.5	52.3	195	4 Q96E93	Q96E93 homo sapien
5	525.5	50.7	189	4 Q43198	Q43198 homo sapien
6	201.5	19.4	275	11 Q9D403	Q9D403 mus musculu
7	184	17.8	257	13 Q90636	Q90636 gallus gall
8	178	17.2	181	4 Q9NZS1	Q9NZS1 homo sapien
9	178	17.2	231	4 Q9NZS2	Q9NZS2 homo sapien
10	177.5	17.1	200	13 Q802S8	Q802S8 gallus gall
11	177	17.1	231	6 Q8MI05	Q8MI05 macaca fasc
12	177	17.1	238	11 Q8BRU4	Q8BRU4 mus musculu
13	176.5	17.0	422	6 Q8HY11	Q8HY11 hylobates s
14	175	16.9	179	11 Q54708	Q54708 mus musculu
15	175	16.9	179	11 Q54707	Q54707 mus musculu
16	174.5	16.8	191	4 Q9UHP7	Q9UHP7 homo sapien

17	174.5	16.8	293	11 Q8CBB4	Q8CBB4 mus musculu
18	174.5	16.8	399	6 Q8HY12	Q8HY12 hylobates l
19	174.5	16.8	399	6 Q8HY10	Q8HY10 hylobates c
20	173.5	16.7	208	11 Q91ZW7	Q91ZW7 mus musculu
21	173	16.7	165	11 Q9R007	Q9R007 mus musculu
22	173	16.7	211	11 Q91ZW5	Q91ZW5 mus musculu
23	173	16.7	223	11 Q925G5	Q925G5 mus musculu
24	172	16.6	230	13 Q9PU48	Q9PU48 gallus gall
25	171	16.5	165	6 Q9GLF4	Q9GLF4 sus scrofa
26	170.5	16.5	227	11 Q91V25	Q91V25 mus musculu
27	170.5	16.5	227	11 Q61973	Q61973 mus musculu
28	170	16.4	223	11 Q925G3	Q925G3 mus musculu
29	169.5	16.4	225	4 Q12918	Q12918 homo sapien
30	169.5	16.4	233	6 Q8MJH7	Q8MJH7 pongo pygma
31	168.5	16.3	227	11 Q925G4	Q925G4 mus musculu
32	168.5	16.3	229	4 Q9P126	Q9P126 homo sapien
33	168.5	16.3	233	6 Q8MJH6	Q8MJH6 pongo pygma
34	168.5	16.3	237	11 Q91ZW8	Q91ZW8 mus musculu
35	167.5	16.2	200	6 Q8SPX1	Q8SPX1 sus scrofa
36	167.5	16.2	233	6 Q8MJ10	Q8MJ10 pongo pygma
37	167	16.1	217	11 Q64228	Q64228 mus sp. nkl
38	167	16.1	223	11 Q99P32	Q99P32 mus musculu
39	167	16.1	223	11 Q99JB4	Q99JB4 mus musculu
40	166	16.0	223	11 Q7TMP8	Q7TMP8 mus musculu
41	166	16.0	236	6 Q95L94	Q95L94 macaca mula
42	165.5	16.0	164	11 Q8BL24	Q8BL24 mus musculu
43	165.5	16.0	229	11 Q9JL99	Q9JL99 mus musculu
44	165.5	16.0	233	6 Q8MJH8	Q8MJH8 pongo pygma
45	165.5	16.0	376	6 Q8HY06	Q8HY06 gorilla gor

ALIGNMENTS

RESULT 1

ID	Q64335	PRELIMINARY;	PRT;	188 AA.
AC	Q64335;			
DT	01-NOV-1996	(TrEMBLrel. 01, Created)		
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	MAFA protein.			
GN	MAFA.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN=SPRAGUE DAWLEY; TISSUE=Testis;			
RA	Bocek Jr P., Gutmann M.D., Pecht I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96016176; PubMed=7568140;			
RA	Guthmann M.D., Tal M., Pecht I.;			
RT	"A secretion inhibitory signal transduction molecule on mast cells is another C-type lectin."			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).			
DR	EMBL; X97191; CAA65829.1; -.			
DR	EMBL; X97192; CAA65829.1; JOINED.			
DR	EMBL; X97193; CAA65829.1; JOINED.			
DR	EMBL; X97194; CAA65829.1; JOINED.			
DR	EMBL; X97195; CAA65829.1; JOINED.			
DR	EMBL; X79812; CAA56208.1; -.			
DR	PIR; I59421; I59421.			
DR	GO; GO:0005529; F:sugar binding; IEA.			
DR	InterPro; IPR001304; Lectin_C.			
DR	Pfam; PF000059; lectin_c; 1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00041; C TYPE LECTIN 2; 1.			
SEQ	SEQUENCE 188 AA; 21355 MW; 2CC8032D4D020B15 CRC64;			

Query Match 100.0%; Score 1036; DB 11; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1e-102;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTIVLMSLLLYQRTL 60
 DB 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTIVLMSLLLYQRTL 60

QY 61 CCGSGKGFMCSCRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGSHLLTFFPDQGVN 120
 DB 61 CCGSGKGFMCSCRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGSHLLTFFPDQGVN 120

QY 121 LFOEYVGEDFWIGLRIDGWRWEDGPALSLISLSNSVVKCGTHRCGLHASSCEVALQ 180
 DB 121 LFOEYVGEDFWIGLRIDGWRWEDGPALSLISLSNSVVKCGTHRCGLHASSCEVALQ 180

QY 181 WICEKVL 188
 DB 181 WICEKVL 188

RESULT 2

O88713 PRELIMINARY; PRT; 188 AA.

ID O88713
 AC O88713;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-AUG-1999 (TREMELrel. 11, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor G1).
 GN KLIG1 OR MAFA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C.B-17 SCID;
 RX MEDLINE=99077194; PubMed=9862378;
 RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
 RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
 RL Eur. J. Immunol. 28:4409-4417(1998).
 RN [2]
 RP SEQUENCE OF 2-188 FROM N.A.
 RA Blaser C.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
 RX MEDLINE=21115136; PubMed=11220622;
 RA Voehringer D., Kaufmann M., Pircher H.;
 RT "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLIG1), the mouse homologue of MAFA";
 RL Immunogenetics 52:206-211(2001).
 DR EMBL; AF097357; AAD03718.1; -;
 DR EMBL; AF010751; CAA09342.1; -;
 DR EMBL; AF317727; AAK40082.1; -;
 DR MGB; MGI:135294; Klrg1.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 KW Lectin; Receptor.
 SQ SEQUENCE 188 AA; 21396 MW; 876336802EAL34F1 CRC64;

Query Match 80.9%; Score 838; DB 11; Length 188;
 Best Local Similarity 80.7%; Pred. No. 1.6e-81;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTIVLMSLLLYQRTL 60
 DB 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTIVLMSLLLYQRTL 60

QY 61 CCGSGKGFMCSCRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGSHLLTFFPDQGVN 120
 DB 61 CCGSKDSTCSHCPCPILMTENGSHCYFFSMKRDWNSLKFCADKSGSHLLTFFPDQGVN 120

QY 121 LFOEYVGEDFWIGLRIDGWRWEDGPALSLISLSNSVVKCGTHRCGLHASSCEVALQ 180
 DB 121 LFEYLGDFWIGLRIDGWRWEDGPALSLISLSNSVVKCGTHRCGLHASSCEVALQ 180

QY 181 WICEKVL 187
 DB 181 WICKKVL 187

RESULT 3
 O75613
 ID O75613 PRELIMINARY; PRT; 189 AA.

AC O75613;
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE ITIM-containing receptor MAFA-L.
 GN MAFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Butcher S., Arney K.L., Cook G.P.;
 RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene complex and expressed by basophils and NK cells.";
 RL Eur. J. Immunol. 28:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077194; PubMed=9862378;
 RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
 RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
 RL Eur. J. Immunol. 28:4409-4417(1998).
 DR EMBL; AF081675; AAC32200.1; -;
 DR EMBL; AF097358; AAD03719.1; -;
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match 52.7%; Score 545.5; DB 4; Length 189;
 Best Local Similarity 55.1%; Pred. No. 3.1e-50;
 Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTIVLMSLLLYQRTL 60
 DB 1 MTDSVIYSMLELPTATQANDYGPQKSSSRPSCSLVALGLTAVLLSVLLYQWIL 60

QY 61 CCGSGKGFMCSCRCPNLWMRNGSHCYFFSMKRDWNSLKFCADKSGSHLLTFFPDQGVN 120
 DB 61 CGSGNSTCASPCPCDRWKMVGNHCYFFSVEKRDWNSLFLCLARDSHLLVITDQWMS 120

QY 121 LFOEYVGEDFWIGLRIDGWRWEDGPALSLISLSNSVVKCGTHRCGLHASSCEVALQ 179
 DB 121 LLQVFLSEAFWIGLRNNSGWRWEDGSPINFSRISNSFVQTCGAINKNGLOASSCEVALQ 180

QY 180 QWICEKV 186
 DB 181 HWCKKV 187


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RESULT 4
Q96E93 ID Q96E93 PRELIMINARY; PRT; 195 AA.
AC Q96E93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to killer cell lectin-like receptor subfamily G, member 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012621; AAH12621.1; -.
DR Genew; HGNC:6380; KLRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
KW Lactin; Receptor.
SQ SEQUENCE 195 AA; 21831 MW; 178E98B08EEC473 CRC64;

Query Match 52.3%; Score 541.5; DB 4; Length 195;
Best Local Similarity 54.8%; Pred. No. 8.6e-50;
Matches 102; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDSDRWKAVLHRPCVSYLVNVALGLLTAVILMSLLYLQRTL 60
DB 1 MTDSVIYSMLELPTATQAQNDYGPQKSSSSKSCCLVAITGLLTAVILSVLLYQWIL 60

QY 61 CGSGKGFMCQSCRCPLNMRNGSHCYFFSMKRDWNSLKPCADKSGHLLTPPDNGVN 120
DB 61 CGGSNTSTCASCPCPDPRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNGMS 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPAISLS-ILNSVVKCGTTHRCGLHASSCEVAL 179
DB 121 LLQVFUSEAFCWIGLRNNSGWRWEDGSPFNFSRISNSFVQTCGAINKNGQLASSCEVPL 180

QY 180 QWICEK 185
DB 181 HWVCKK 186

Query Match 52.3%; Score 541.5; DB 4; Length 195;
Best Local Similarity 54.8%; Pred. No. 8.6e-50;
Matches 102; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDSDRWKAVLHRPCVSYLVNVALGLLTAVILMSLLYLQRTL 60
DB 1 MTDSVIYSMLELPTATQAQNDYGPQKSSSSKSCCLVAITGLLTAVILSVLLYQWIL 60

QY 61 CGSGKGFMCQSCRCPLNMRNGSHCYFFSMKRDWNSLKPCADKSGHLLTPPDNGVN 120
DB 61 CGGSNTSTCASCPCPDPRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNGMS 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPAISLS-ILNSVVKCGTTHRCGLHASSCEVAL 179
DB 121 LLQVFUSEAFCWIGLRNNSGWRWEDGSPFNFSRISNSFVQTCGAINKNGQLASSCEVPL 180

QY 180 QWICEK 185
DB 181 HWVCKK 186

RESULT 5
O43198 ID O43198 PRELIMINARY; PRT; 189 AA.
AC O43198;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAPA has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212(1998).
DR EMBL; AF034952; AAC34731.1; -.

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DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0003793; F:defense/immunity protein activity; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;

Query Match 50.7%; Score 525.5; DB 4; Length 189;
Best Local Similarity 53.5%; Pred. No. 4.3e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDSDRWKAVLHRPCVSYLVNVALGLLTAVILMSLLYLQRTL 60
DB 1 MTDSVIYSMLELPTATQAQNDYGPQKSSSSKSCCLVAITGLLTAVILSVLLYQWIL 60

QY 61 CGSGKGFMCQSCRCPLNMRNGSHCYFFSMKRDWNSLKPCADKSGHLLTPPDNGVN 120
DB 61 CGGSNTSTCASCPCPDPRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNGMS 120

QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPAISLS-ILNSVVKCGTTHRCGLHASSCEVAL 179
DB 121 LLQVFUSEAFCWIGLRNNSGWRWEDGSPFNFSRISNSFVQTCGAINKNGQLASSCEVPL 180

QY 180 QWICEK 186
DB 181 HGVCCKV 187

RESULT 6
Q9D403 ID Q9D403 PRELIMINARY; PRT; 275 AA.
AC Q9D403;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 4933425B16Rik protein.
GN 4933425B16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK016908; BAB30491.1; -.
DR HSSP; P23807; IIXX.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN NCBI_TaxID=9606;
[1]
RX MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
RA Fernandez-Ruiz E.;
RT "Human KLRFL, a novel member of the killer cell lectin-like receptor
RT gene family: molecular characterization, genomic structure, physical
RT mapping to the NK gene complex and expression analysis.";
RL Eur. J. Immunol. 30:568-576(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=21150889; PubMed=11265639;
RA Vitale M., Falco M., Castriiconi R., Parolini S., Zambello R.,
RA Semenzato G., Biassoni R., Bottino C., Moretta L., Moretta A.;
RT "Identification of NKp80, a novel triggering molecule expressed by
RT human natural killer cells.";
RL Eur. J. Immunol. 31:233-242(2001).
DR EMBL; AF175206; AAF37804.1; -.
DR EMBL; AJ305370; CAC29425.1; -.
DR Genew; HGNC:13342; KLRFL.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. .; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 231 AA; 26562 MW; A2F7BE6D4341AFDE CRC64;

Query Match 17.2%; Score 178; DB 4; Length 231;
Best Local Similarity 23.3%; Pred. No. 8.3e-11;
Matches 56; Conservative 34; Mismatches 84; Indels 66; Gaps 11;

QY 1 MADNSYSTLELPAAPRVQ--DSSRWKVK---AVLHRCPCSVLVMVAL-----GLLTIVLM 51
DB 1 MQDEERYMTLNVQSKRSSAQTSLTFKDYSVTLH---WKILLGSGTVNGILTLTLI 56

QY 52 SLLLY-----QRTLC-----CGSKGFCWSCQSCR 75
DB 57 SLLLYSQGVLLKQKSGCSNATQYEDTGLKVNNGTRRNISNKDLCASRS--ADQTVLC 114

QY 76 PNLWMRNGSHCYFYSMEKRDWNSLKFCDKSGHLLTFPPNQGNLFOEYVVG--DFYVIG 134
DB 115 QSEWLKYGQCYWFNSNEMKSWSDSYVYCLERKSHLLIHLHOLEMAFLQKNLRQINLVYVIG 174

QY 135 LRID---GMRWEDGPALSIL-----SNSVVKCGTHRCGLHASSCEVALOWICE 184
DB 175 LNFETSLKMTWTWVDGSPIDSKIPFKGPAKENS-----CAAIKESKIPSETCSSVFKWICQ 230

RESULT 10
ID Q80258 PRELIMINARY; PRT; 200 AA.
AC Q80258;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-type lectin.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,

RA Kaiser P.;
RT "Analysis of part of the chicken Rfp-Y region reveals two novel lectin
RT genes, the first complete genomic sequence of a class I alpha-chain
RT gene, a truncated class II beta-chain gene, and a large CRI repeat.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277927; CAD61336.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; lectin_C.
DR Pfam; PF00059; lectin.c; 1.
DR PRINTS; PR00356; ANTI-FREZEII.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 200 AA; 22573 MW; 23AA950D11334988 CRC64;

Query Match 17.1%; Score 177.5; DB 13; Length 200;
Best Local Similarity 26.1%; Pred. No. 7.9e-11;
Matches 42; Conservative 24; Mismatches 66; Indels 29; Gaps 5;

QY 39 VMVALGLLTIVLMSLLLYORTLCCGSKGFCWSCQ-----CSRCPLNLMRNGSHCYF 89
DB 41 VCAALGALLILVLVI-----STVCRQVPVPPFPDFAHACPNAAWVGQKCYF 88

QY 90 SMEKRDWNSLKFCDKSGHLLTFPPNQGNLFOEYVVGDFYVIGL---RDIDGWRWEDG 146
DB 89 SKEENDWNSRHCNAHAGSLATIGSAEEMFMRFQGPANCWIGLHREEDAQWTWSDG 148

QY 147 PALS---LSILSNSVVKCGTHRCGLHASSCEVALOWICEK 185
DB 149 TAFTNWFEIRGGG---RCAYLNGDRISSLSLCHLKHVWVCSR 186

RESULT 11
ID Q8MI05 PRELIMINARY; PRT; 231 AA.
AC Q8MI05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NKp80 NK receptor.
GN NKp80.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NK lymphocytes;
RA Biassoni R.;
RT "Macaca fascicularis NK cell and receptors.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ426430; CAD19994.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; lectin_C.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 231 AA; 26710 MW; 403C79CA68893C1E7 CRC64;

Query Match 17.1%; Score 177; DB 6; Length 231;
Best Local Similarity 23.5%; Pred. No. 1.1e-10;
Matches 56; Conservative 32; Mismatches 88; Indels 62; Gaps 10;

QY 1 MADNSYSTLELPAAPRVQDSSRW-----KVKAVLHRCPCSVLVMVAL-----GLLTIVLM 51
DB 1 MQDEERYMTLNVQSKKRTSTQTLTFKDYSVVLH---WKILLGSGTLGILALALI 56

QY 52 SLLLY---QRTLCGSKGF-----MC-----SQCSRCPN 77

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Db 57 SLILLVSGVLLKCKGSHNSHTTETHDGLKMNNGTRNTSNKDLVSRADQTVLCQS 116
QY 78 LWMRNGSHCYFVSMEKRDWNSLKFCADKGGSHLLTFPPNQGNVLFQEVYVGEDFY-WIGLR 136
Db 117 EWLKYGKCYWFSNEMKSWSDSYVYCLBRKSHLLTIQDELEMAFTQKNLRQSNYVWMLN 176
QY 137 DID---GWRWEDGPALSLSL-----SNSVVKCGTTHRCGLHASSCEVALQWICE 184
Db 177 FTSLKMTWTWVDGSLDPKIFIKGPAKENS-----CAAIKSKIYSETCSSVFKWICQ 230

RESULT 12
Q8BRU4
ID Q8BRU4 PRELIMINARY; PRT; 238 AA.
AC Q8BRU4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical C-type lectin domain containing protein.
GN 9830005G06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK041288; BAC30890.1; -.
DR MGD; MGI:2444608; 9830005G06RIK.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeZell.
DR IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 27014 MW; 07368A0380B95EAL CRC64;

Query Match 17.1%; Score 177; DB 11; Length 238;
Best Local Similarity 25.7%; Pred. No. 1.1e-10;
Matches 63; Conservative 30; Mismatches 78; Indels 74; Gaps 12;

QY 1 MADNSIYSTL--ELP---AAPRVQDSR-----WKVKAVLHRPCVSYLVWVALGILL-TVIL 50
Db 1 MHAEIYTSLOWDIPTEASQKSPSKGAWCVVTMI--SCV-----VCMGLLATSIF 53
QY 51 MSL-----LQYRTLCGSKGFMCSQ 71
Db 54 LGIKFFQVSSVLVQERLIQDALTALVNLQWQRYTLEYCQALLQSLHSG-----SD 107
QY 72 CSRCPNLWMRNGSHCYFVSMEKRDWNSLKFCADKGGSHLLTFPPNQGNVLFQ---EYVGE 128
Db 108 CSPCPHNWQNGKSCYVFERWEMWNISKKSLKEGASLFQDSKEEMEFTSIIGKLKGG 167
QY 129 DFYWIGLRDIDG---NRWEDGPALSLSL-----SNSVVKCGTTHRCGLHASSCEVALQ 180
Db 168 NKYVWGVFQ-DGISGSFWEDGSSPLSDLPAPQRSAQGIKDKSTLISDKDSWKY 226
QY 181 WICEK 185
Db 227 FICEK 231
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RESULT 13

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Q8HY11
ID Q8HY11 PRELIMINARY; PRT; 422 AA.
AC Q8HY11;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative CD209L1 protein.
GN CD209L1.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1533;
RX PubMed=12477827;
RA Bashirova A.A.; Wu L.; Cheng J.; Martin T.D.; Martin M.P.;
RA Benveniste R.E.; Lifson J.D.; Kewallamani V.N.; Hughes A.;
RA Carrington M.;
RT "Novel Member of the CD209 (DC-SIGN) Gene Family in Primates.";
RL J. Virol. 77:217-227 (2003).
DR EMBL; AY078820; AAL89529.1; -.
DR EMBL; AY078814; AAL89529.1; JOINED.
DR EMBL; AY078815; AAL89529.1; JOINED.
DR EMBL; AY078816; AAL89529.1; JOINED.
DR EMBL; AY078817; AAL89529.1; JOINED.
DR EMBL; AY078818; AAL89529.1; JOINED.
DR EMBL; AY078819; AAL89529.1; JOINED.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeZell.
DR IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 422 AA; 48031 MW; 1F24460CBF991DC3 CRC64;

Query Match 17.0%; Score 176.5; DB 6; Length 422;
Best Local Similarity 29.9%; Pred. No. 2.5e-10;
Matches 38; Conservative 19; Mismatches 57; Indels 13; Gaps 3;

QY 72 CSRCPNLWMRNGSHCYFVSMEKRDWNSLKFCADKGGSHLLTFPPNQGNVLFQEVYVGED-- 129
Db 288 CCRCPKDWTTFQGNCYFMSNSQRNWHDSVTACQEVAGLQVLVKSAEQNFLOQTSRNR 347
QY 130 FYWIGLRDID---GWRWEDGPALSLSL-----SNSVVKCGTTHRCGLHASSCEVA 178
Db 348 FSWMGLSDLAQEGTWQVDGSPLSSTSFQRYWNSGEPNNSGDCAEFSGSGMNDRCNVD 407
QY 179 LOWICEK 185
Db 408 NYWICKX 414

RESULT 14
Q54708
ID Q54708 PRELIMINARY; PRT; 179 AA.
AC Q54708;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD94.
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB.17 SCID;
RX MEDLINE=98124458; PubMed=9464811;
RA Vance R.E.; Tanamachi D.M.; Hanke T.; Raullet D.H.;
```

```
RT "Cloning of a mouse homolog of CD94 extends the family of C-type
RT lectins on murine natural killer cells.;"
RL Eur. J. Immunol. 27:3236-3241(1997).
DR EMBL; AF030312; AAC28244.1; -.
DR MGD; MGI:1196275; Klrd1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF like.
DR DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS0041; C TYPE LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SQ SEQUENCE 179 AA; 20809 MW; D59ELCB63139B45 CRC64;

Query Match 16.9%; Score 175; DB 11; Length 179;
Best Local Similarity 27.9%; Pred. No. 1.3e-10;
Matches 50; Conservative 36; Mismatches 71; Indels 22; Gaps 10;

QY 22 SRWKVAVLHR-PCVSYLVNVALGLLTIVILMSLLLYQRTLC-CGSKGFM-CSQCSRCPNL 78
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
7 TRWRLMSVIFGIKCL--FLMVTILGVLLINSFTIQISTPSTPTTTFVQFVSECCVCLDK 64

QY 79 WMENGSHCYFYSMEKRDWNSLKFCADKSGSHLLTTPDNOGVNLFQBYVVGEDFYWIGL--- 135
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
65 WVGHCNCYFISKEKSWERSRDFCASQNSLLQ--PQSRNELSFMNF-SQTFEFGMHYS 122

QY 136 RDIDGHRWEDGPALSILSN-SVQKCGTIHRC-----GLHASSCEVALQWICEKV 186
Db :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
123 EKENAMLWEDGTVPKDLFPFVSIRP---EHCIVVSPSKSVSAESCKENKRYICKL 177

Search completed: August 10, 2004, 16:18:50
Job time : 33.6089 secs

RESULT 15
O54707 PRELIMINARY; PRT; 179 AA.
AC O54707;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
GN KLRD1 OR CD94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Vance R.B., Tanamachi D.M., Hanke T., Raullet D.H.;
RL Eur. J. Immunol. 27:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
RT "Murine CD94.;"
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Butcher S., Cottage A., Cook G.P.;
RT "Mouse natural killer cell receptors homologous to human CD94 and
RT NKG2-D.;"
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030311; AAC28243.1; -.
DR EMBL; AF057714; AAC33713.1; -.
DR EMBL; AF039025; AAD02116.1; -.
DR MGD; MGI:1196275; Klrd1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:05:01 ; Search time 46.5841 Seconds
(without alignments)
1140.281 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSIYSYILELPAPRVQD.....GLHSSCEVALQWICEKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1036	100.0	188	2 AAR77033	Mammalian
2	1036	100.0	188	2 AAW88277	Rat mast
3	1036	100.0	188	4 AAE11761	Rat mast
4	838	80.9	188	4 AAE11760	Mouse mas
5	651	62.8	114	2 AAR77472	Partial s
6	545.5	52.7	189	7 ADD25635	Binding d
7	525.5	50.7	189	2 AAW88265	Human mas
8	525.5	50.7	189	4 AAE11759	Human mas
9	418.5	40.4	843	4 ABG05451	Novel hum
10	251.5	24.3	191	6 ABJ37898	NOVX prot
11	207.5	20.0	99	2 AAW88267	Human MAF
12	184.5	17.8	199	2 AAW54659	Human CD6
13	184.5	17.8	199	2 AAW85593	Human CD6
14	184.5	17.8	199	7 ADD25621	Binding d
15	184	17.8	257	2 AAW85594	Chicken 1
16	183	17.7	228	4 AAU02495	Human sec
17	182	17.6	268	6 ABJ19328	NOVX rela
18	182	17.6	276	6 ABR43190	Human REM
19	182	17.6	276	6 AAE37769	Human C-t
20	180	17.4	231	5 ABB81897	Human Nkp
21	179.5	17.3	241	7 ADE07884	Novel pro
22	179.5	17.3	265	4 AAU19657	Human nov
23	179.5	17.3	265	5 ABP47877	Human pol
24	179.5	17.3	265	7 ADC10839	Human ext
25	179.5	17.3	275	6 ABJ19327	NOVX rela

ALIGNMENTS

RESULT 1

AAR77033
ID AAR77033 standard; protein; 188 AA.

XX AAR77033;

DT 01-FEB-1996 (first entry)

DE Mammalian mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA; soluble; ligand;

KW identification; screening; inflammation; inflammatory; allergy; allergic;

KW prevention.

XX Rattus rattus.

XX WO9527734-A1.

PD 19-OCT-1995.

XX 06-APR-1995; 95WO-US004258.

XX 08-APR-1994; 94IL-00109257.

XX (YEDA) YEDA RES & DEV CO LTD.
(RYCU//) RYCUS A.

PI Pecht I, Guthmann MD, Tal M;

DR WPI; 1995-366356/47.

DR N-PSDB; AAT01471.

XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
useful for screening for ligands of MAFA which are useful for prevention
of inflammatory and allergic reactions.

PS Claim 12; Page 37; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
produced by recombinant techniques for use in the ligand- screening
assay. The ligands that are identified may be used alone or in
combination with the MAFA to prevent inflammatory and allergic reactions

SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;

Best Local Similarity 100.0%; Pred. No. 1.8e-96;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Abr43189 Human REM
Ray66765 Membrane-
Aau12432 Human PRO
Aab65288 Human PRO
Abp43587 Membrane
Abu59103 Human PRO
Abu59181 Novel hum
Abu82693 Human sec
Abol17876 Novel hum
Abu60612 Human sec
Abu13994 Human PRO
Abu81130 Human PRO
Abu72579 Novel hum
Abu66830 Human PRO
Abr39424 Human GEN
Abu59911 Novel sec
Abu59328 Human sec
Abo26025 Human PRO
Abo25101 Human sec
Abu59034 Human sec

26 179.5 17.3 295 6 ABR43189
27 177.5 17.1 229 3 AAY66765
28 177.5 17.1 229 4 AAU12432
29 177.5 17.1 229 4 AAB65288
30 177.5 17.1 229 5 ABP43587
31 177.5 17.1 229 6 ABUS8103
32 177.5 17.1 229 6 ABUS9181
33 177.5 17.1 229 6 ABUS2693
34 177.5 17.1 229 6 ABO17876
35 177.5 17.1 229 6 ABUS60612
36 177.5 17.1 229 6 ABUI3994
37 177.5 17.1 229 6 ABUI8130
38 177.5 17.1 229 6 ABUI72579
39 177.5 17.1 229 6 ABUS66830
40 177.5 17.1 229 6 ABR39424
41 177.5 17.1 229 6 ABUS9911
42 177.5 17.1 229 6 ABUS9328
43 177.5 17.1 229 6 ABO26025
44 177.5 17.1 229 6 ABO25101
45 177.5 17.1 229 6 ABUS9034

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 DB 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 QY 61 CCGSGKGFMCSCQSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDNQGYN 120
 DB 61 CCGSGKGFMCSCQSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDNQGYN 120
 QY 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 DB 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 QY 181 WICEKVLP 188
 DB 181 WICEKVLP 188
 RESULT 2
 AAW88277
 ID AAW88277 standard; protein; 188 AA.
 AC AAW88277;
 DT 29-MAR-1999 (first entry)
 DE
 DE Mast cell function-associated antigen (MAFA).
 KW Mast cell function-associated antigen; MAFA; splice variant; rat;
 KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
 XX
 OS Rattus sp.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 82..84
 FT Modified-site /note= "Asn is N-glycosylated"
 FT Modified-site 97..99
 FT Modified-site /note= "Asn is N-glycosylated"
 XX
 PN WO9854209-A2.
 XX
 PD 03-DEC-1998.
 XX
 PF 29-MAY-1998; 98WO-GB001572.
 XX
 PR 31-MAY-1997; 97GB-00011148.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
 PI WPI; 1999-059806/05.
 XX
 DR N-PSDB; AAV84222.
 DR
 DR New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.
 XX
 XX Disclosure; Fig 4; 44pp; English.
 XX
 CC This is the amino acid sequence of rat mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
 CC basophils. The invention relates to cloning of the human MAFA molecule
 CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
 CC of human MAFA that are not found in rat. Polypeptides and synthetic
 CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
 CC and polynucleotides encoding them, can be used in methods for the
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
 CC arthritis and asthma), and tumour growth
 XX
 SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1.8e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 DB 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMMVALGLLTVILMSLLLYQRTL 60
 QY 61 CCGSGKGFMCSCQSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDNQGYN 120
 DB 61 CCGSGKGFMCSCQSRCPNLWMRNGSHCYFFSMKRDWNSLKFCDKDGSHLLTFPDNQGYN 120
 QY 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 DB 121 LFOEYVVGDFYWGILRDIDGWRWEDGPALSLSILSNSVVKCGTTHRCGLHASSCEVALQ 180
 QY 181 WICEKVLP 188
 DB 181 WICEKVLP 188
 RESULT 3
 AAEL1761
 ID AAEL1761 standard; protein; 188 AA.
 AC AAEL1761;
 DT 18-DEC-2001 (first entry)
 DE
 DE Rat mast cell function associated antigen (MAFA) protein.
 XX
 KW Rat; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 XX Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 DR N-PSDB; AAD18736.
 DR
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 XX Example 1; Page 19; 49pp; English.
 XX
 CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is rat MAFA protein

XX SQ Sequence 188 AA;
 Query Match 100.0%; Score 1036; DB 4; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1.8e-96;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MADNSYSTLELPAAAPRVQDSSRWKAVLHRRPCVSYLVNVALGILLTVILMSLLLYORTL 60
 DB 1 MADNSYSTLELPAAAPRVQDSSRWKAVLHRRPCVSYLVNVALGILLTVILMSLLLYORTL 60
 QY 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFFSMKRDWNSLSLKFCADKGSHELLTTPDNOGVN 120
 DB 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFFSMKRDWNSLSLKFCADKGSHELLTTPDNOGVN 120
 QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKGTIHRCGLHASSCEVALQ 180
 DB 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKGTIHRCGLHASSCEVALQ 180
 QY 181 WICEKVL 188
 DB 181 WICEKVL 188
 RESULT 4
 AAE11760
 ID AAE11760 standard; protein; 188 AA.
 XX AC AAE11760;
 DT 18-DEC-2001 (first entry)
 XX DE Mouse mast cell function associated antigen (MAFA) protein.
 XX KW Mouse; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 FT Domain 64..188
 FT /note= "Extracellular domain"
 XX WO200170805-A2.
 XX 27-SEP-2001.
 XX 16-MAR-2001; 2001WO-US008596.
 XX 17-MAR-2000; 2000US-0190716P.
 XX (GEMI-) GEMINI SCI INC.
 XX Takahashi N, Mikayama T;
 XX WPI; 2001-611482/70.
 XX N-PSDB; AAD18735.
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX Example 1; Page 19; 49pp; English.
 XX The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition

CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein
 XX SQ Sequence 188 AA;
 Query Match 80.9%; Score 838; DB 4; Length 188;
 Best Local Similarity 80.7%; Pred. No. 1.9e-76;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
 QY 1 MADNSYSTLELPAAAPRVQDSSRWKAVLHRRPCVSYLVNVALGILLTVILMSLLLYORTL 60
 DB 1 MADSSYSTLELPAPQVQDESQKLVKAVLHRRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
 QY 61 CCGSKGFMCSQCRCPNLWNRNGSHCYFFSMKRDWNSLSLKFCADKGSHELLTTPDNOGVN 120
 DB 61 CCGSKDSTCHPCSCFILWTRNGSHCYFFSMKRDWNSLSLKFCADKGSHELLTTPDNOGVK 120
 QY 121 LFOEYVGEDFYWIGLRIDGWRWEDGPALSLSLNSVVKGTIHRCGLHASSCEVALQ 180
 DB 121 LFGXYLGQDFYWIGLRNIDGWRWEGGPALSLRLTNSLIQRCGAIHRNGLQASSCEVALQ 180
 QY 181 WICEKVL 187
 DB 181 WICKKVL 187
 RESULT 5
 AAR77472
 ID AAR77472 standard; protein; 114 AA.
 XX AC AAR77472;
 DT 01-FEB-1996 (first entry)
 XX DE Partial sequence of mast cell function-associated antigen (MAFA).
 XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;
 KW identification; screening; inflammation; inflammatory; allergy; allergic;
 KW prevention.
 XX OS Rattus rattus.
 XX WO9527734-A1.
 XX 19-OCT-1995.
 XX 06-APR-1995; 95WO-US004258.
 XX 08-APR-1994; 94IL-00109257.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX (RYCU/) RYCUS A.
 XX Pecht I, Guthmann MD, Tal M;
 XX WPI; 1995-366356/47.
 XX N-PSDB; AAT01471.
 XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
 PT useful for screening for ligands of MAFA which are useful for prevention
 PT of inflammatory and allergic reactions.
 XX Disclosure; Page 38; 54pp; English.
 XX A soluble form of mast cell function-associated antigen (MAFA) can be
 CC produced by recombinant techniques for use in the ligand- screening
 CC assay. The ligands that are identified may be used alone or in
 CC combination with the MAFA to prevent inflammatory and allergic reactions

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XX SQ Sequence 114 AA;
Query Match 62.8%; Score 651; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-58;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFQEVYVGDYFWIG 134
DB 1 CPNLWRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGNLFQEVYVGDYFWIG 60

QY 135 LRDIDGWRWEDGPAISLSILNSVQKQGTIHRGCLHASSCEVALQWICEKVL 188
DB 61 LRDIDGWRWEDGPAISLSILNSVQKQGTIHRGCLHASSCEVALQWICEKVL 114

RESULT 6
ADD25635 standard; protein; 189 AA.
XX AC
XX AC ADD25635;
XX DT
XX DT 15-JAN-2004 (first entry)
XX DE Binding domain-immunoglobulin fusion protein-associated protein #95.
XX KW Binding domain; immunoglobulin; fusion protein; cytostatic;
XX KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
XX KW neuroprotective; hinge region; immunoglobulin heavy chain;
XX KW CH2 constant region; CH3 constant region; IgG1;
XX KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
XX KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
XX KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX OS Unidentified.
XX FN US2003118592-A1.
XX PD 26-JUN-2003.
XX PF 25-JUL-2002; 2002US-00207655.
XX PR 17-JAN-2001; 2001US-0367358P.
XX PR 17-JAN-2002; 2002US-00053530.
XX PR 03-JUN-2002; 2002US-0385691P.
XX PA (GENE-) GENE-CRAFT INC.
XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX DR WPI; 2003-801317/75.
XX PT New binding domain-immunoglobulin fusion protein, useful for treating a
XX PT subject having or suspected of having a malignant condition or a B-cell
XX PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX PS Disclosure; SEQ ID NO 196; 157pp; English.
XX CC The invention relates to a binding domain-immunoglobulin fusion protein
XX CC comprising a binding domain polypeptide that is fused to an
XX CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CC CH2 constant region polypeptide that is fused to the hinge region
XX CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX CC polypeptide that is fused to the CH2 constant region polypeptide. The
XX CC hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin
XX CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
XX CC region polypeptide, derived from (a) having 3 or more cysteine residues;
XX CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
XX CC contains 2 cysteine residues, where the first cysteine is not mutated; a
XX CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
XX CC (a) having 3 or more cysteine residues, where the mutated human IgG1
XX CC immunoglobulin hinge region polypeptide contains no more than one
cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
polypeptide, derived from (a) having 3 or more cysteine residues; where
the mutated human IgG1 immunoglobulin hinge region polypeptide contains
no cysteine residues. The binding domain-immunoglobulin fusion protein is
capable of at least one immunological activity comprising antibody
dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
binding domain polypeptide is capable of specifically binding to an
antigen. Also included are an isolated polynucleotide encoding the
binding domain-immunoglobulin fusion protein, a recombinant expression
construct comprising the polynucleotide (operably linked to a promoter),
a host cell transformed or transfected with a recombinant expression
construct, producing the binding domain-immunoglobulin fusion protein, a
pharmaceutical composition comprising the binding domain-immunoglobulin
fusion protein or polynucleotide and a carrier, and treating a subject
having or suspected of having a malignant condition or a B-cell disorder.
The binding domain-immunoglobulin fusion protein is useful for treating a
subject having or suspected of having a malignant condition or a B-cell
disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
sclerosis or autoimmune disease. The present sequence is a binding domain
-immunoglobulin fusion protein-associated protein sequence. Note: The
sequence data for this patent formed part of the printed specification
and is also available in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
identified the sequences in the printed specification by their SEQ ID
number therefore none of the sequences can be explicitly identified.
XX SQ Sequence 189 AA;
Query Match 52.7%; Score 545.5; DB 7; Length 189;
Best Local Similarity 55.1%; Pred. No. 7.1e-47;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYVSTLELPAPRVQDDSRWKVAVLHPCVSYLVVALGLTLVILMSLLLYQRTL 60
DB 1 MTSVIYVSMLELPTAQNDYGPQKSSSRSPSCSLVALGTLAVLSVLLYQWIL 60

QY 61 CCGSKGFMCSCRCPNLWNRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGN 120
DB 61 CQGSNYSTCASCPCSPDRWKYGNHCYFVSVEEKDWNSSLEFLCLARDSHLLVITDQMS 120

QY 121 LFOBYVGEDFYWIGLRDIDGWRWEDGPAISLS-ILNSVQKQGTIHRGCLHASSCEVAL 179
DB 121 LLQVFLSEAFWCIGLRNNSGWRWEDGSPNLSRISNSFVQTCGAINKNGIQAASCEVPL 180

QY 180 QWICEKV 186
DB 181 HWVCKV 187

RESULT 7
AAW88265 standard; protein; 189 AA.
XX AC
XX AC AAW88265;
XX DT
XX DT 29-MAR-1999 (first entry)
XX DE Human mast cell function-associated antigen (MAFA).
XX KW Mast cell function-associated antigen; MAFA; splice variant; human;
XX KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 7..10
XX FT Modified-site 65..67
XX FT Modified-site 97..99
XX FT Modified-site 137..139

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XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS69638.
XX PF New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX PS Claim 20; SEQ ID NO 35810; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: the sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 843 AA;

Query Match 40.4%; Score 418.5; DB 4; Length 843;
Best Local Similarity 49.4%; Pred. No. 3.1e-33;
Matches 78; Conservative 30; Mismatches 49; Indels 1; Gaps 1;

QY 11 ELPAAPRYDDSRWKKAVLHRCPCVYLVMVALGLLTVLMSLLLYQRTLCGSGKGFMS 70
Db 665 ELPTATQNDYGPQOKSSRRPSCSLVALALGLLTAVLLSVLLYQWILCOGSNYSTCA 724
QY 71 QCSRCPNLWMRNGSHCYFFSMEKRDWNSSLKFCADKGSLLTFFPDNQGVNLFQEXVVGEDF 130
Db 725 SCPCSCFDRWKKYGNHCYFFSVEEKDWNSSLEFCLARDSHLLVITTDNQEMSLQLVFLSEAF 784
QY 131 YWIGLRDIDGWREDGPAISLSILSN-SVQKCGTIHR 167
Db 785 CWIGLRNNSGWRWEDGSLNFSRNTNGTIIRKRKLHK 822

RESULT 10
ABU37898
ID ABU37898 standard; protein; 191 AA.

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XX AC ABU37898;
XX DT 22-MAY-2003 (first entry)
XX DE NOXV protein sequence SEQ ID No 42.
XX KW Hepatotropic; immunosuppressive; cardiact; hypertensive; tranquilizer;
KW vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic;
KW antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
KW anticonvulsant; antiaddictive; analgesic; dermatological; keratolytic;
KW antiseborrheic; antirheumatic; antiarthritic; antinflammatory; anti-HIV;
KW cytostatic; antiasthmatic; antipsoriatic; hypotensive; osteopathic;
KW antiulcer; anorectic; antidiabetic; antiallergic; haemostatic;
KW neuroleptic; antidepressant; antifertility; NOXV; human disease;
KW NOXV-associated disorder; trauma; viral; bacterial; fungal; protozoal;
KW parasitic infection; Alzheimer's disease; stroke; forensic biology;
KW immunogen; non-human transgenic animal; gene therapy.
XX OS Unidentified.
XX PN WO200281517-A2.
XX PD 17-OCT-2002.
XX PF 22-JAN-2002; 2002WO-US002064.
XX PR 19-JAN-2001; 2001US-0262892P.
XX PR 23-JAN-2001; 2001US-0263598P.
XX PR 24-JAN-2001; 2001US-0263799P.
XX PR 25-JAN-2001; 2001US-0264117P.
XX PR 25-JAN-2001; 2001US-0264139P.
XX PR 26-JAN-2001; 2001US-0264478P.
XX PR 30-JAN-2001; 2001US-0263351P.
XX PR 02-MAR-2001; 2001US-0272870P.
XX PR 14-MAR-2001; 2001US-0275927P.
XX PR 14-MAR-2001; 2001US-0275990P.
XX PR 15-MAR-2001; 2001US-0276449P.
XX PR 20-MAR-2001; 2001US-0277358P.
XX PR 23-MAR-2001; 2001US-0278151P.
XX PR 29-MAR-2001; 2001US-0279857P.
XX PR 20-APR-2001; 2001US-0285140P.
XX PR 30-APR-2001; 2001US-0285141P.
XX PR 17-MAY-2001; 2001US-0287484P.
XX PR 08-JUN-2001; 2001US-0291701P.
XX PR 10-JUL-2001; 2001US-0304353P.
XX PR 12-JUL-2001; 2001US-0304355P.
XX PR 09-AUG-2001; 2001US-0311289P.
XX PR 13-AUG-2001; 2001US-0311975P.
XX PR 16-AUG-2001; 2001US-0312937P.
XX PR 18-OCT-2001; 2001US-0330227P.
XX PR 29-NOV-2001; 2001US-0334198P.
XX PA (CURA-) CURAGEN CORP.
XX PI Decristofaro MF, Padigaru M, Miller C, Tchernev V, Zhong H;
PI Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastelli L;
PI Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M;
PI Burgess CB, Eisen A, Wolenc A, Baumgartner J, Shinkets RA, Gusev V;
PI Vernet CAM, Taupier RJ, Pena C, Shenoy S, Li L, Casman S, Boldog F;
PI Fernandes E, Smithson G, Malyankar U, Tailon B, Liu X;
XX WPI; 2003-058504/05.
XX DR N-PSDB; AET33363.
XX PT New polypeptides, designated as NOXV, useful for diagnosing and treating
PT infections, neurological diseases, cancer, allergy, and bone,
PT immunological, skin, renal, brain, muscle and autoimmune disorders.
XX PS Claim 1; Page 118; 672pp; English.

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CC The invention relates to a novel isolated polypeptide, designated NOVX
CC (NOV1 - 33), consisting of a mature form of one of 51 sequences, given in
CC the specification, or its variant, where amino acid residue(s) in the
CC variant differ from the mature form, provided that the variant differs in
CC not more than 15 % of the amino acids from the sequence of the mature
CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
CC an antibody to the polypeptides, are useful for treating or preventing a
CC NOVX-associated disorder in humans and for treating a syndrome associated
CC with a human disease (NOVX-associated disorder). NOVX polypeptides and
CC the encoding nucleic acids, are useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX
CC polypeptide and polynucleotide, by measuring the level of polypeptide
CC expression or the amount of nucleic acid from a mammal and comparing it
CC with another mammal not having or not predisposed to the disease. NOVX
CC polypeptide is also useful for identifying an agent that binds to NOVX
CC and a cell expressing NOVX is useful for identifying an agent that
CC modulates the expression or activity of NOVX. The antibodies and a
CC polypeptide having 95 % sequence identity to NOVX polypeptide are useful
CC for treating a pathological state in a mammal. The antibodies are also
CC useful for determining the presence or amount of NOVX in a sample. NOVX
CC polypeptides, polynucleotides and antibodies specific for the
CC polypeptides are useful for treating or preventing disorders or syndromes
CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
CC infections. They can also treat disorders such as e.g., Alzheimer's
CC disease or a stroke. The NOVX encoding nucleic acids are useful for
CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
CC for identifying a cell or tissue type in a biological sample, to amplify
CC DNA sequences from very small biological samples such as tissues e.g.
CC hair or skin or body fluids in forensic biology and as primers and probes
CC for use in identifying and/or cloning NOVX homologues in other cell
CC types. The NOVX proteins are useful as an immunogen to generate
CC antibodies which are useful for diagnostically monitoring protein levels
CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are
CC useful for producing non-human transgenic animals which are useful for
CC studying the function and/or activity of NOVX protein and for identifying
CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic
CC acids can be used in gene therapy. This sequence represents a NOVX
CC protein of the invention

XX SQ Sequence 191 AA;

Query Match 24.3%; Score 251.5; DB 6; Length 191;
Best Local Similarity 31.4%; Pred. No. 3.8e-17;
Matches 59; Conservative 24; Mismatches 84; Indels 21; Gaps 5;
QY 12 LPAPRVQDSDRWKRAVL--HRPCVSY-LVMVALGLLTVILMSLLLYQRTLCGSGKGF 68
Db 12 LPSPQFESHORLVLLPILHVNKSYRMYSFCLGLFTLVROSLSLSPLECSGALSAH 71
QY 69 CSQSCPCPNLWMNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTFFPDNQVNLQBYVGE 128
Db 72 CKICEPCPTSWLFPFGSGCYFYSFKTTWBAQAQGCADASAHLAAFPEDRKVAFYSVLLGR 131
QY 129 DFYWIGLRIDGWRW-----DGPAL--SLSILSNVVKCGTTHRCGLHASSCEVAL 179
Db 132 CLFGLGLARVGGWRVAPGTQIDAFVGGACFCQESI-----SGLPASELRLEK 182
QY 180 QWICEKVL 187
Db 183 WWHCSKTL 190

RESULT 11

AAW88267
ID AAW88267 standard; protein; 99 AA.

XX AC AAW88267;

XX DT 29-MAR-1999 (first entry)

XX DE Human MAPA splice variant huMAFA(E3/4-).

KW Mast cell function-associated antigen; MAPA; huMAFA(E3/4-);
KW splice variant; human; inflammation; allergy; asthma;
KW rheumatoid arthritis; tumour; therapy.

OS Homo sapiens.

PN WO9854209-A2.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB001572.

XX PR 31-MAY-1997; 97GB-00011148.

XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX DR WPI; 1999-059806/05.

XX DR N-PSDB; AAV84200.

XX New polypeptide having a sequence corresponding to human mast cell
XX function-associated antigen - useful in forming and manufacturing
XX pharmaceutical compositions in the treatment of inflammatory and allergic
XX diseases, and tumour growth.

PS Disclosure; Fig 3; 44pp; English.

XX This is the amino acid sequence of human mast cell function- associated
XX antigen (MAPA) splice variant huMAFA(E3/4-), which lacks the C-lectin-
XX like domain of human MAPA (see AAW88265) but retains the intracellular
XX and transmembrane domains as well as the extracellular C-terminal tail.
XX Truncated MAPA polypeptides including huMAFA(E3/4-), and polynucleotides
XX encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-
XX 72), can be used in compositions for the treatment of
XX inflammatory and allergic diseases (e.g. rheumatoid arthritis and
XX asthma), or tumour growth

XX SQ Sequence 99 AA;

Query Match 20.0%; Score 207.5; DB 2; Length 99;
Best Local Similarity 29.6%; Pred. No. 4.7e-13;
Matches 55; Conservative 12; Mismatches 30; Indels 89; Gaps 1;
QY 1 MADNSTYSTLELPAPRPVQDSDRWKRAVLHRCVSYLVMVALGLLTVILMSLLLYQRTL 60
Db 1 MTDSVIYSMLLELPATQAQNDYGPQQKSSSRPSCSLVAIALGLLTAVLLSVLLYQWIL 60
QY 61 CCGSKGFCMCSQCRCPCNLWMNGSHCYFYSMEKRDWNSLSLKFCADKGSLLTFFPDNQVN 120
Db 61 CQG-----
QY 121 LFOEYVGEDFYWIGLRDIDGWRWEDGPFALSLSILSNVVKCGTTHRCGLHASSCEVALQ 180
Db 64 -----ISSNSFVQTCGATKNGIQASSCEVPLH 91

QY 181 WICEKV 186

Db 92 WVCKV 97

RESULT 12

AAW54659

ID AAR54659 standard; protein; 199 AA.

XX AC AAR54659;

XX DT 25-MAR-2003 (revised)

XX DT 31-OCT-1994 (first entry)

XX DE Human CD69.

KW Immune system; thrombocyte development; signal transduction; probe;

KW assay; diagnosis; therapy.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Protein 79..199
FT /note= "soluble polypeptide"
XX
XX
PN W09410188-A1.
XX
PD 11-MAY-1994.
XX
XX 28-OCT-1993; 93WO-US010418.
PF
XX 29-OCT-1992; 92US-00971097.
PR
XX (IMMV) IMMUNEX CORP.
PA
XX Ziegler SR, Hjerrild KA;
PI
XX WPI; 1994-167377/20.
DR N-PSDB; AAQ65340.
XX
XX CD69 nucleic acids and polypeptide - used in the diagnosis, therapy and
FT study of the activation and regulation of the immune system.
PT
XX
XX Claim 10; Page 27; 35pp; English.
PS
XX The sequence is that of human CD69. The CD69 protein is active in the
CC regulation and function of the immune system. The protein may be used for
CC blocking thymocyte development in in vitro systems. The soluble
CC polypeptide can be used to competitively bind the ligand in vivo thus
CC inhibiting signal transduction activity via endogenous cell surface bound
CC CD69. CD69 may also be used to generate antibodies. See also AAR54660.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 199 AA;

Query Match 17.8%; Score 184.5; DB 2; Length 199;
Best Local Similarity 26.3%; Pred. No. 2.4e-10;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
QY 35 VSYLVVALGLLTILMSLLLYQRTLCGSGKFC---SQSRCPNLMWRNGSHCYFPM 91
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
45 VMNVVFTILLIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQKCYFIST 101
QY 92 EKRDNWSLKPCADKGSLLTFFPDNQGNLFQEVYGEDFYWIGLRIDG--WRWEDGPAL 149
Db || | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKPKPGHPKWSNGKEF 161
QY 150 SLSTLSNSVVKCGTIHRCGLHASSCEVALOWICEK 185
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
162 N-NWFNVGTGDKCVFLKNTVEVSMCEKNLYWICNK 196

RESULT 13
AAW85593
ID AAW85593 standard; protein; 199 AA.
XX
AC AAW85593;
XX
DT 02-MAR-1999 (first entry)
XX
DB Human CD69.
XX
KW lectin; carbohydrate; binding; agglutination; selectin; receptor;
KW calcium dependent binding; treatment; cancer; detection; identification;
KW CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
XX
OS Homo sapiens.
XX
XX W09849306-A1.
FN
XX

PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US008791.
XX
PR 29-APR-1997; 97US-00846523.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Shah P;
XX
XX WPI; 1999-024060/02.
DR N-PSDB; AAV83109.
XX
PT New human C-type lectin and related nucleic acid, vectors, transformed
PT cells - antibodies, agonists and antagonists, for diagnosis, prevention
PT and treatment of cancers.
XX
PS Example 3; Page 48; 64pp; English.
XX
XX Human CD69 shows homology with the human CTL-1 protein sequence.
CC Recombinant cells containing expression vectors comprising the CTL-1
CC coding sequence can be used to produce recombinant CTL-1 which is useful
CC for raising Ab and to screen for specific binding agents. Binding agents
CC which are antagonists of CTL-1 can be used to treat or prevent cancer,
CC e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are
CC associated with overexpression of CTL-1. Fragments of this sequence are
CC used to diagnose these conditions, as probes or primers in usual
CC hybridisation and/or amplification assays, or for gene mapping, while
CC complements of this sequence, antisense or ribozyme sequences are used to
CC treat or prevent the aforementioned cancers also. Ab are used directly as
CC antagonists or for delivery of therapeutic agents to cells that express
CC CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
CC also a transmembrane domain, but no secretory signal. CTL-1 also shows
CC homology with chicken 17.5.3 (AAW85594), and mouse CD69 (AAW85595)
XX
XX proteins
SQ Sequence 199 AA;

Query Match 17.8%; Score 184.5; DB 2; Length 199;
Best Local Similarity 26.3%; Pred. No. 2.4e-10;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
QY 35 VSYLVVALGLLTILMSLLLYQRTLCGSGKFC---SQSRCPNLMWRNGSHCYFPM 91
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
45 VMNVVFTILLIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQKCYFIST 101
QY 92 EKRDNWSLKPCADKGSLLTFFPDNQGNLFQEVYGEDFYWIGLRIDG--WRWEDGPAL 149
Db || | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREHVVGLKPKPGHPKWSNGKEF 161
QY 150 SLSTLSNSVVKCGTIHRCGLHASSCEVALOWICEK 185
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
162 N-NWFNVGTGDKCVFLKNTVEVSMCEKNLYWICNK 196

RESULT 14
ADD25621
ID ADD25621 standard; protein; 199 AA.
XX
AC ADD25621;
XX
DT 15-JAN-2004 (first entry)
XX
DB Binding domain-immunoglobulin fusion protein-associated protein #88.
XX
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritis; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX OS Unidentified.
 XX PN US2003118592-A1.
 XX XX 26-JUN-2003.
 XX PF 25-JUL-2002; 2002US-00207655.
 XX XX 17-JAN-2001; 2001US-0367358P.
 XX PR 17-JAN-2002; 2002US-00053530.
 XX PR 03-JUN-2002; 2002US-0385691P.
 XX XX (GENE-) GENE-CRAFT INC.
 XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX XX WPI; 2003-801317/75.
 XX XX New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX XX Disclosure; SEQ ID NO 182; 157pp; English.
 XX XX The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide; derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.
 XX XX Sequence 199 AA;
 XX SQ Query Match 17.8%; Score 184.5; DB 7; Length 199;
 XX Best Local Similarity 26.3%; Pred. No. 2.4e-10;
 XX Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;
 XX 35 VSYLVNVALGLAVILMSILLYQRTLCGSGKFWC---SQSCRCPNLWNGSHCYFSM 91

Db 45 VMNVFTILIALISVGQYN--CPGQYTFMPSDSDSHVSSCEDWVGQRCYFIST 101
 Qy 92 EKRDWNSLXFCADKSGHLLTFPDNQGVNLFQEVYGEDFYWIGLRDIDG--WRWEDGPA 149
 Db 102 VKRSWTSAQNACSEHGATLAVIDSEKDMNFKRYAGREHWHVGLKKEPGHPKWSNGKEF 161
 Qy 150 SLSILSNSVVKCGTHIRCGLHASSCEVALQWICEK 185
 Db 162 N-NWFNVTGSDKCVFLKXNTEVSSMECEKNLYWICNK 196

RESULT 15
 AAW85594
 ID AAW85594 standard; protein; 257 AA.
 XX AC AAW85594;
 XX AC
 XX DT 17-OCT-2003 (revised)
 XX DT 02-MAR-1999 (first entry)
 XX XX
 XX DE Chicken 17.5.3 protein.
 XX XX
 XX KW lectin; carbohydrate; binding; agglutination; selectin; receptor;
 KW calcium dependent binding; treatment; cancer; detection; identification;
 KW CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.
 XX OS Gallus gallus.
 XX PN WO9849306-A1.
 XX XX
 XX PD 05-NOV-1998.
 XX XX
 XX PF 29-APR-1998; 98WO-US0008791.
 XX XX
 XX PR 29-APR-1997; 97US-00846523.
 XX XX
 XX PA (INCY-) INCYTE PHARM INC.
 XX XX
 XX PI Bandman O, Shah P;
 XX XX
 XX DR WPI; 1999-024060/02.
 XX DR N-PSDB; AAV83109.
 XX XX
 XX PT New human C-type lectin and related nucleic acid, vectors, transformed
 PT cells - antibodies, agonists and antagonists, for diagnosis, prevention
 PT and treatment of cancers.
 XX XX
 XX PS Example 3; Page 48-49; 64pp; English.
 XX XX
 XX CC Chicken 17.5.3 protein shows homology with the human CTL-1 protein.
 CC Recombinant cells containing expression vectors comprising the CTL-1
 CC coding sequence can be used to produce recombinant CTL-1 which is useful
 CC for raising Ab and to screen for specific binding agents. Binding agents
 CC which are antagonists of CTL-1 can be used to treat or prevent cancer,
 CC e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are
 CC associated with overexpression of CTL-1. Fragments of this sequence are
 CC used to diagnose these conditions, as probes or primers in usual
 CC hybridisation and/or amplification assays, or for gene mapping, while
 CC complements of this sequence, antisense or ribozyme sequences are used to
 CC treat or prevent the aforementioned cancers also. Ab are used directly as
 CC antagonists or for delivery of therapeutic agents to cells that express
 CC CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa35-149) and
 CC also a transmembrane domain, but no secretory signal. CTL-1 also shows
 CC homology with human CD69 (AAW85593), and mouse CD69 (AAW85595) proteins.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX XX
 XX SQ Sequence 257 AA;
 XX Query Match 17.8%; Score 184; DB 2; Length 257;
 XX Best Local Similarity 28.6%; Pred. No. 3.7e-10;
 XX Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

33	QY	PCVSYLVWVALGLLT	VILMSLLLYQRTLC	CGSGKFMCSQC	SRPNLWNRNSHC	YIYPSME	92	
		: :	: :	: :	: :	: :		
101	Db	PC-----	MLVLAVAVIL----	QDSCSPRPF-----	SHVCNANWV	FOCKCYFSDT	146	
		: :	: :	: :	: :	: :		
93	QY	KRDWNSLKC	CAKDGSHLLTF	PNQGNVL	FOEYVGEDFY	IGLRDIDG----	WRNEDGPA	149
		: :	: :	: :	: :	: :		
147	Db	ESDWSNSR	CHRGILGAS	LATLDTKEEN	EFMLQYQRP	ADRWIGLHRA	EGDEHWTWADG	206
		: :	: :	: :	: :	: :		
150	QY	SLSILSNSVQ	-----	KCGTIIHRC	GLHASSCEVA	LQWICEK	185	
		: :	: :	: :	: :	: :		
207	Db	T-----	NRPEFLRGGG	CAYLNGDGI	SALCKSEK	FWCVR	243	
		: :	: :	: :	: :	: :		

Search completed: August 10, 2004, 16:16:29
Job time : 47.5841 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:18:53 ; Search time 40.2619 Seconds
(without alignments)
1464.718 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036

Sequence: 1 MADNSYSTLELPAPRVQD.....GLHASSCEVALQWICKVLP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	9	US-09-811-367B-5
2	838	80.9	188	9	US-09-811-367B-3
3	545.5	52.7	189	14	US-10-207-655-196
4	525.5	50.7	189	9	US-09-811-367B-1
5	184.5	17.8	199	10	US-09-284-320-86
6	184.5	17.8	199	14	US-10-207-655-182
7	184.5	17.8	199	14	US-10-179-528-3
8	184.5	17.8	199	15	US-10-379-127-26
9	184	17.8	257	14	US-10-179-528-4
10	182	17.6	268	15	US-10-161-493-22
11	180	17.4	231	16	US-10-451-843-1
12	179.5	17.3	265	9	US-09-764-870-307
13	179.5	17.3	265	4	US-10-125-540-307
14	179.5	17.3	275	15	US-10-161-493-20
15	177.5	17.1	229	9	US-09-989-722-424

16	177.5	17.1	229	9	US-09-989-723-424	Sequence 424, App
17	177.5	17.1	229	9	US-09-989-279-424	Sequence 424, App
18	177.5	17.1	229	9	US-09-989-727-424	Sequence 424, App
19	177.5	17.1	229	9	US-09-989-731-424	Sequence 424, App
20	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
21	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
22	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
23	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
24	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
25	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
26	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
27	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
28	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
29	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
30	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
31	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
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33	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
34	177.5	17.1	229	9	US-09-989-732-424	Sequence 424, App
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36	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
37	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
38	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
39	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
40	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
41	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
42	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
43	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
44	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App
45	177.5	17.1	229	10	US-09-989-734-424	Sequence 424, App

ALIGNMENTS

RESULT 1

US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811.367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match 100.0%; Score 1036; DB 9; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.7e-99;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	CCSGKFCMCSQRCNLRNWSHCYFYSMEKRDWNSLKFCADKXGSHLLTFPDNOGVN	120
Db	61	CCSGKFCMCSQRCNLRNWSHCYFYSMEKRDWNSLKFCADKXGSHLLTFPDNOGVN	120
Qy	121	LFOEYVGEDFYWITGLRIDGWRWEDGPALSLSTLSNSVVKCGTTHRCGHHASSCEVALQ	180
Db	121	LFOEYVGEDFYWITGLRIDGWRWEDGPALSLSTLSNSVVKCGTTHRCGHHASSCEVALQ	180

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QY 181 WICKVLP 188
Db 181 WICKVLP 188

RESULT 2
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 80.9%; Score 838; DB 9; Length 188;
Best Local Similarity 80.7%; Pred. No. 9.7e-79;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

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Db 1 MADSSIYSTLELPAAPRVQDDSRWKVAVLHRPPLSRFAMVALGLLTVILMSLLMYQRL 60

QY 61 CCGSGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
Db 61 CCGSKDSTGSHPCPILWTRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVK 120

QY 121 LFOEYVGEDFYWIGLRDIDGWRWDGPALSLSLNSVVKCGTHRCGLHASSCEVALQ 180
Db 121 LFGELYGQDFYWIGLRNIDGWEGGAPALSLRLTNSLQRCGAIHRNGLQASSCEVALQ 180

QY 181 WICKVLP 187
Db 181 WICKVLP 187

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match 52.7%; Score 545.5; DB 14; Length 189;
Best Local Similarity 55.1%; Pred. No. 2.3e-48;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

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QY 61 CCGSGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
Db 61 CQGSNYSTASCPCPDRCWKMKGNYHYFYSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

QY 121 LFOEYVGEDFYWIGLRDIDGWRWDGPALSLSLNSVVKCGTHRCGLHASSCEVAL 179
Db 121 LLQVFLSEAFWCWIGLRNNSGWRWDGSPNLSRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 180 QWICEKV 186
Db 181 HWCKKV 187

RESULT 4
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1

Query Match 50.7%; Score 525.5; DB 9; Length 189;
Best Local Similarity 53.5%; Pred. No. 2.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHRPCVSYLVVVALGLLTVILMSLLLYQRTL 60
Db 1 MTDSVIYSMLLELPTAQNDYGPQKSSSSRSPSCCLVAITGLLTAVALLSVLLYQWIL 60

QY 61 CCGSGFMCSCQRCPNLWMRNGSHCYFYSMEKRDWNSLKFCAKDGSHLLTFPDNQGVN 120
Db 61 CQGSNYSTASCPCPDRCWKMKGNYHYFYSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

QY 121 LFOEYVGEDFYWIGLRDIDGWRWDGPALSLSLNSVVKCGTHRCGLHASSCEVAL 179
Db 121 LLQVFLSEAFWCWIGLRNNSGWRWDGSPNLSRISNSFVQTCGAINKNGLOASSCEVPL 180

QY 180 QWICEKV 186
Db 181 HWCKKV 187

RESULT 5
US-09-284-320-86
; Sequence 86, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seiichi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
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; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-86

Query Match      17.8%; Score 184.5; DB 10; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVWVALGLLTVILMSLLLYQRTLCGSGKGMFC---SQCRCPNLWMRNGSHCYFMS 91
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Db 45 VMNVVFITILIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQYQKCYFIST 101
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 92 EKRDWNSLKFCDKADKSHLLTFDPNQGVNLFQEVVGDFYWGILRDIDG--WRWEDGPAL 149
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREEHWGLKPEGHPKWSNGKEF 161
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 150 SLSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 162 N-NWNVVTGSKCVFLKNTVSSMECEKNLYWICNK 196
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 6
US-10-207-655-182
; Sequence 182, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 182
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-182

Query Match      17.8%; Score 184.5; DB 14; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVWVALGLLTVILMSLLLYQRTLCGSGKGMFC---SQCRCPNLWMRNGSHCYFMS 91
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
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QY 92 EKRDWNSLKFCDKADKSHLLTFDPNQGVNLFQEVVGDFYWGILRDIDG--WRWEDGPAL 149
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREEHWGLKPEGHPKWSNGKEF 161
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 150 SLSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 162 N-NWNVVTGSKCVFLKNTVSSMECEKNLYWICNK 196
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 7
US-10-179-528-3
; Sequence 3, Application US/10179528
; Publication No. US20030166136A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQUENCES: 7
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/179,528
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,523
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0281 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 291898
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-179-528-3

Query Match      17.8%; Score 184.5; DB 14; Length 199;
Best Local Similarity 26.3%; Pred. No. 7.2e-11;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVWVALGLLTVILMSLLLYQRTLCGSGKGMFC---SQCRCPNLWMRNGSHCYFMS 91
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 45 VMNVVFITILIALISVGQYN---CPGQYTFSPSDSHVSSCSDEDWVGQYQKCYFIST 101
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 92 EKRDWNSLKFCDKADKSHLLTFDPNQGVNLFQEVVGDFYWGILRDIDG--WRWEDGPAL 149
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Db 102 VKRSWTSQAQACSEHGATLAVIDSEKDMNFKRYAGREEHWGLKPEGHPKWSNGKEF 161
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 150 SLSILSNVVKCGTTHRCGLHASSCEVALQWICEK 185
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 162 N-NWNVVTGSKCVFLKNTVSSMECEKNLYWICNK 196
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 8
US-10-379-127-26
; Sequence 26, Application US/10379127
; Publication No. US20040005592A1
; GENERAL INFORMATION:
; APPLICANT: Emtage, Peter C.R.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Goodrich, Ryle
; APPLICANT: Tang, Y. Ton
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAR
; FILE REFERENCE: NUVO-01CIP
; CURRENT APPLICATION NUMBER: US/10/379,127
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 299
; SEQ ID NO 20
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-493-20

Query Match      17.3%   Score 179.5; DB 15; Length 275;
Best Local Similarity 31.5%; Pred. No. 3.5e-10;
Matches 41; Conservative 22; Mismatches 56; Indels 11; Gaps 5;

Qy      67  FMCQSCRCPLNMRNGSHCYFSM-EKRDWNSSLKFCADKSGSHLLTFP--DNQGVNLFQ 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      135  FSDHRCNPPCKMOWQNSCYFTTNEEKTWANGKDCIDKNSTLVKIDSLSEKDFLMSQ 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      124  EYVGEDFYWIGLR-DIDG--WRWEDGPALSLSILNSNVQ-----KGTIHRCGLHASSC 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      195  PLLMFSFFWLGLSWDSSGRSFWEDGVPSPSLSTKELDQINGSGKCAIFQKGNIIYISRC 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      176  BVALQWICEK 185
      : : : : :
Db      255  SAEIFWICEK 264
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RESULT 15
US-09-989-722-424
; Sequence 424, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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76  PNLWMRNGSHCYFSMEKRDWNSSLKFCADKSGSHLLTFPDNQGVNL-----PQEVVGEDFY 131
138  PNNWIONRSCYYVSEIWSIWHTSQENCLKEGSLTLQTESKEEMDFITGSLRKIKGSVDY 197
132  WIGLRDIDG----WRWEDGPALSLSIL-----SNSVWQKGTIHRCGLHASSCEVALOWIC 183
198  WGLSQ-DGHSRGLMWQGSFSPGLLPAERSQANQVGVKNSLLSSNCSWKYFIC 256
184  EK 185
257  EK 258

RESULT 14
US-10-161-493-20
; Sequence 20, Application US/10161493
; Publication No. US20040018555A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Gorman, Linda
; APPLICANT: Pena, Carol EA
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leite, Mario W
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Miller, Charles E
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Hjalit, Tord
; APPLICANT: Voss, Edward Z
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Ji, Weizhen
; APPLICANT: Smithson, Glenda
; APPLICANT: Edinger, Salomit R
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; TITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypepti
; FILE REFERENCE: 21402-377A
; CURRENT APPLICATION NUMBER: US/10/161,493
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/337,524
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/359,151
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
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; PRIOR FILING DATE: 2001-12-14
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; PRIOR FILING DATE: 2001-06-12
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? PRIOR FILING DATE: 1998-04-28
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? PRIOR APPLICATION NUMBER: 60/087106
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? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089538
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089598
? PRIOR FILING DATE: 1998-06-17
? PRIOR APPLICATION NUMBER: 60/089599

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.6407 Seconds
(without alignments)
662.924 Million cell updates/sec

Title: US-09-811-367B-5
Perfect score: 1036
Sequence: 1 MADNSIYSLTLPAPRVQD.....GLHASSCEVALQWICKVLP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
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3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	3	US-08-722-126A-5
2	1036	100.0	188	5	PCT-US95-04258-5
3	651	62.8	114	3	US-08-722-126A-6
4	651	62.8	114	5	PCT-US95-04258-6
5	273	26.4	76	4	US-09-531-056A-23
6	184.5	17.8	199	5	PCT-US93-10418-2
7	175.5	16.9	199	3	US-08-772-440-13
8	175.5	16.9	229	4	US-09-247-155-97
9	174.5	16.8	191	4	US-09-531-056A-6
10	169.5	16.4	225	2	US-08-738-462-2
11	169.5	16.4	225	5	PCT-US94-07587-2
12	166.5	16.1	115	3	US-08-722-126A-8
13	166.5	16.1	115	5	PCT-US95-04258-8
14	166.5	16.1	190	4	US-09-127-946-14
15	164.5	15.9	273	3	US-09-111-470-10
16	164.5	15.9	292	2	US-08-688-342-4
17	164.5	15.9	292	2	US-09-113-788-4
18	164.5	15.9	316	3	US-09-111-470-4
19	161.5	15.6	194	4	US-09-531-056A-2
20	161.5	15.6	201	2	US-08-688-342-1
21	161.5	15.6	201	2	US-09-113-788-1
22	158.5	15.3	167	3	US-08-772-440-21
23	158.5	15.3	209	3	US-08-772-440-4
24	158	15.3	1487	3	US-08-840-062-7
25	157	15.2	216	3	US-08-543-246B-9
26	157	15.2	216	3	US-08-543-246B-24
27	157	15.2	328	4	US-09-531-056A-13

28 155 15.0 179 1 US-08-690-095-9 Sequence 9, Appli
29 155 15.0 179 2 US-08-650-578-2 Sequence 2, Appli
30 155 15.0 179 2 US-08-688-342-3 Sequence 3, Appli
31 155 15.0 179 2 US-09-113-788-3 Sequence 3, Appli
32 155 15.0 179 3 US-09-113-789-9 Sequence 9, Appli
33 154 14.9 199 5 PCT-US93-10418-4 Sequence 4, Appli
34 153.5 14.8 404 4 US-09-517-605-2 Sequence 2, Appli
35 153 14.8 122 3 US-08-722-126A-9 Sequence 9, Appli
36 153 14.8 122 5 PCT-US95-04258-9 Sequence 9, Appli
37 153 14.8 126 3 US-08-772-440-10 Sequence 10, Appli
38 153 14.8 134 3 US-08-543-246B-20 Sequence 20, Appli
39 153 14.8 176 3 US-08-772-440-8 Sequence 8, Appli
40 153 14.8 180 3 US-08-772-440-31 Sequence 31, Appli
41 153 14.8 187 4 US-09-127-946-12 Sequence 12, Appli
42 153 14.8 244 3 US-08-772-440-2 Sequence 2, Appli
43 149.5 14.4 168 3 US-08-772-440-17 Sequence 17, Appli
44 148 14.3 173 4 US-09-531-056A-4 Sequence 4, Appli
45 148 14.3 237 3 US-09-111-470-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5
Query Match 100.0%; Score 1036; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.3e-105;

	Matches	188;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTIVILMSLLLYQRTL	60							
Db	1	MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTIVILMSLLLYQRTL	60							
Qy	61	CCSGKGPMSQCSCRCPNLWRNGSHCYFFSMEKEDWNSSLKFCADKSGHLLTFPDNQGVN	120							
Db	61	CCSGKGPMSQCSCRCPNLWRNGSHCYFFSMEKEDWNSSLKFCADKSGHLLTFPDNQGVN	120							
Qy	121	LFQYEVGEDFYWIGLRLDIDGWRWEDGPALSLSILSNSVVOKCGTTHRCGLHASSCEVALQ	180							
Db	121	LFQYEVGEDFYWIGLRLDIDGWRWEDGPALSLSILSNSVVOKCGTTHRCGLHASSCEVALQ	180							
Qy	181	WICEKVLPL 188								
Db	181	WICEKVLPL 188								

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1 RESULT 2
2 PCT-US95-04258-5
3 ; Sequence 5, Application PC/TUS9504258
4 ; GENERAL INFORMATION:
5 ; APPLICANT:
6 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
7 ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
8 ; NUMBER OF SEQUENCES: 10
9 ; CORRESPONDENCE ADDRESS:
10 ; ADDRESSEE: BROWDY AND NEIMARK
11 ; STREET: 419 Seventh Street, N.W., Suite 300
12 ; CITY: Washington
13 ; STATE: D.C.
14 ; COUNTRY: USA
15 ; ZIP: 20004
16 ; COMPUTER READABLE FORM:
17 ; MEDIUM TYPE: Floppy disk
18 ; COMPUTER: IBM PC compatible
19 ; OPERATING SYSTEM: PC-DOS/MS-DOS
20 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
21 ; CURRENT APPLICATION DATA:
22 ; APPLICATION NUMBER: PCT/US95/04258
23 ; FILING DATE: 06-APR-1995
24 ; PRIOR APPLICATION DATA:
25 ; APPLICATION NUMBER: IL 109257
26 ; FILING DATE: 08-APR-1994
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: BROWDY, Roger L.
29 ; REGISTRATION NUMBER: 25,618
30 ; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: 202-628-5197
33 ; TELEFAX: 202-737-3528
34 ; TELEX: 248633
35 ; INFORMATION FOR SEQ ID NO: 5:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 188 amino acids
38 ; TYPE: amino acid
39 ; TOPOLOGY: linear
40 ; MOLECULE TYPE: protein
41 PCT-US95-04258-5

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121 LFEQYVGGDFYWGILRDIIDGWRWEDGPALSLSILSNSVVKCGCTIHRCGLHASCEVALQ 181
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121 LFEQYVGGDFYWGILRDIIDGWRWEDGPALSLSILSNSVVKCGCTIHRCGLHASCEVALQ 180
|||||

181 WICEKVLP 188
|||||
181 WICEKVLP 188
|||||

RESULT 3
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996

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RESULT 4
PCT-US95-04258-6

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Query Match          26.4%; Score 273; DB 4; Length 76;
Best Local Similarity 59.7%; Pred.No.1.4e-22;
Matches 43; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 75 CPNLWRNNGSHCYFFSMKEKDDWNSSLKFCADKGSHLLTFPDNGVNLFOBYVGEDFWIG 134
Db 3 CPDRWKYGNHCYFFSVEEKDWNSSLEFLCLARDSHLLVITDNOEMSLLOVFLSEAFCWIG 62
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 135 LRIDIGRWEDG 146
Db 63 LRNSGWRWEDG 74
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
PCT-US93-10418-2
; Sequence 2, Application PC/TUS9310418
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Hjerrild, Kathryn A.
; TITLE OF INVENTION: Activation Antigen CD69
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10418
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2610-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-10418-2

Query Match          17.8%; Score 184.5; DB 5; Length 199;
Best Local Similarity 26.3%; Pred.No.2.4e-12;
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSYLVNVALGLLTVILMSLLLYQRTLCCSGKGFMC---SQCSRCPNLWNRNGSHCYFFSM 91
Db 45 VMNVFVITLITALLSQQN---CPQYVTFSPSDSHVSSCEDSWVGYQRKCYFIST 101
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 92 EKRDWNSSLKFCADKGSHLLTFPDNGVNLFOBYVGEDFYWIGLRIDG--WRWEDGPAL 149
Db 102 VKKSWTSQAQACSEHGATLAVIDSEKMNFLKRYAGREHHVGLKKEPGHPKWSNGKEF 161
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 150 SLSILSNSVQKGTTHRCGLHASSCEVALQWICEK 185
Db 162 N-NWPNVTGSDRCVFLKNTVSSMECEKNLYICNK 196
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RESULT 7
US-08-772-440-13
; Sequence 13, Application US/08772440
; Patent No. 6046158

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GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-13

Query Match 16.9%; Score 175.5; DB 3; Length 199;
Best Local Similarity 26.2%; Pred. No. 2.3e-11;
Matches 53; Conservative 32; Mismatches 74; Indels 43; Gaps 11;
QY 7 YSTLEPAAPRVQD-----DSRWKVKAVLHRCPCVSYLVMAVGLL--TVILMSLLLYOR 58
Db 20 FSTQDIHKPRSEKSRAPSPW-----RP-----IAGVLGILCFVVVVAAVL--- 64
QY 59 TLCCGSKGPMQCSCRCPLNWRNGSHCYFFSMEKRDWNSLKFCAADKGSLLTTPDNQG 118
Db 65 ----GALGFGSQSC--LPN-WIMHGKSCYLFSGNSWYSGSRKHCSQLGAHLLKIDNSKE 117
QY 119 VMLFQRYVGE---DFWYIGU--RDIDG-WRWEDGPA-----LSLSILSNSVVKCGTI 165
Db 118 FEFIESQTSRRINAFWIGLSRNQSGPWFWDGSAFFPNSFOVRTVPQESILLHCWVI 177
QY 166 HRCGLHASSCEVALQWICEKV 187
Db 178 HGSEVYNQICNTSSYSICEKEL 199

RESULT 8
US-09-247-155-97
; Sequence 97, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET 021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09

; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 97
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 47...1
US-09-247-155-97

Query Match 16.9%; Score 175.5; DB 4; Length 229;
Best Local Similarity 26.9%; Pred. No. 2.8e-11;
Matches 61; Conservative 32; Mismatches 83; Indels 51; Gaps 12;
QY 1 MADNSIYSTLEL---PAAPRVQDSDR--WKVKA-VLHRCPCVSYLV-MVALGLLTVILMS 52
Db 1 MDEDEGYITLNIKTRKPAIVSVGPASFWWRVMAILLILLCVMVVGLVALGIWSVMQRN 60
QY 53 LLLYQRTLCCGS-----KG-FMCSQCSRCPLNWRNGSHCYFFSMEK 93
Db 61 YLDENENRTGTLOQAKRFCCYVYVQSELKGTFFKGHKCPCDTNRYYYGDSYGFRRHN 120
QY 94 RDWNSLKFCAADKGSLLTTPDNQGVNLFQEVVGBDFY---WGL---RDIDGWRWEDGP 147
Db 121 LTWEESKQVCTDMNATLLKI-DNRNI---VEYIKARTHLIRWVGLSRQKSNEVWKWEDG- 175
QY 148 ALSLSILSNSVVO-----KCGTIHRCGLHASSCEVALQWICEK 185
Db 176 ----SVISENMFLEDEKGNMNCAYFHNGKMHPTFCENKHYLMCER 218

RESULT 9
US-09-531-056A-6
; Sequence 6, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-6

Query Match 16.8%; Score 174.5; DB 4; Length 191;
Best Local Similarity 25.8%; Pred. No. 2.8e-11;
Matches 48; Conservative 29; Mismatches 84; Indels 25; Gaps 6;
QY 11 ELPAAPRVQDSDRWKVKAVLHRCPCVSYLVMAVGLLTVILMSLL--LYQRTLCCGSKGPM 68
Db 15 ELPANPGCLHSKEHSIKATL-----IWRLLFFLIMFTIIVCGMVAALSRAIRANCHQPSV 69
QY 69 CSQCSCRCPLNWRNGSHCYFFSMEKRDWNSLKFCAADKGSLLTTPDNQGVNLFQRYVGE 128
Db 70 CLQAA--CPESWIGFORKCFYFSDTKNWTSSORFCDSDADLAQVESFQELNLLRYKGP 128
QY 129 DFYWIGLRDIDG--WRWEDG-----PALSLSILSNSVVKCGTIHRCGLHASSCEVAL 179
Db 129 SDHWIGLSREQQPPKMWINGTWTROFPILGAG-----ECAYLNDKGASSARHYTER 180

Qy 180 QWICEK 185
 Db 181 KWICSK 186

RESULT 10

US-08-738-462-2
 ; Sequence 2, Application US/08738462
 ; Patent No. 5965401
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Chiwen
 ; APPLICANT: Lanier, Lewis L.
 ; APPLICANT: Phillips Jr., Joseph H.
 ; TITLE OF INVENTION: Purified Mammalian NK Antigens and
 ; TITLE OF INVENTION: Related Reagents
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/738,462
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/093,435
 ; FILING DATE: 16-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0397
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-852-9196
 ; TELEFAX: 415-496-1200
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 225 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-738-462-2

Query Match 16.4%; Score 169.5; DB 2; Length 225;
 Best Local Similarity 26.1%; Pred. No. 1.2e-10;
 Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;
 Qy 1 MADNSIYSTLELP-----AAPR-VQDDSRKVKAVLRPC--VSYLVMVALGLL 46
 Db 1 MDQAIYAEINLPDTS GPSSPSLPRDVCGSPWH-QFALKUSCAGIILLVLTG-L 58
 Qy 47 TVILMSLLYQRTLCCKSGKGMCSQCS-----RCPNLMWRNGSHCYF 89
 Db 59 SVSVTSLI--QKS-----SIEKCSVDIQSRNKTTERPGLLNCPIYWQQLREKCLLF 108
 Qy 90 SMEKRDWNSSLKFCADKSGHLLTPDQGNVLFQYVGED--FWIGLR---DIDGRWE 144
 Db 109 SHTVPMNNSLADCTKESLLLRDKDELHTQNLIRDKAILFWIGLNFSLSEKNKWI 168
 Qy 145 DGPALS---LSILSNSVVKCGTTHRCGLHASSCEVALOWICEKVL 187
 Db 169 NGSFLNSNDLEIRGDAXENSCISISQTSVYSEYSTEIRWICQKEL 214
 RESULT 11
 PCT-US94-07587-2

; Sequence 2, Application PC/TUS9407587
 ; GENERAL INFORMATION:
 ; APPLICANT: Schering Corp.
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND
 ; TITLE OF INVENTION: RELATED REAGENTS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schering Corp.
 ; STREET: One Giralda Farms
 ; CITY: Madison
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07940
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.1
 ; SOFTWARE: Microsoft Word 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07587
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lunn, Paul G.
 ; REGISTRATION NUMBER: 32,743
 ; REFERENCE/DOCKET NUMBER: DX0397K
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-822-7255
 ; TELEFAX: 201-822-7039
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 225 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US94-07587-2

Query Match 16.4%; Score 169.5; DB 5; Length 225;
 Best Local Similarity 26.1%; Pred. No. 1.2e-10;
 Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;
 Qy 1 MADNSIYSTLELP-----AAPR-VQDDSRKVKAVLRPC--VSYLVMVALGLL 46
 Db 1 MDQAIYAEINLPDTS GPSSPSLPRDVCGSPWH-QFALKUSCAGIILLVLTG-L 58
 Qy 47 TVILMSLLYQRTLCCKSGKGMCSQCS-----RCPNLMWRNGSHCYF 89
 Db 59 SVSVTSLI--QKS-----SIEKCSVDIQSRNKTTERPGLLNCPIYWQQLREKCLLF 108
 Qy 90 SMEKRDWNSSLKFCADKSGHLLTPDQGNVLFQYVGED--FWIGLR---DIDGRWE 144
 Db 109 SHTVPMNNSLADCTKESLLLRDKDELHTQNLIRDKAILFWIGLNFSLSEKNKWI 168
 Qy 145 DGPALS---LSILSNSVVKCGTTHRCGLHASSCEVALOWICEKVL 187
 Db 169 NGSFLNSNDLEIRGDAXENSCISISQTSVYSEYSTEIRWICQKEL 214
 RESULT 12
 US-08-722-126A-8
 ; Sequence 8, Application US/08722126A
 ; Patent No. 6034227
 ; GENERAL INFORMATION:
 ; APPLICANT: PECHT, Israel
 ; APPLICANT: GUTHMANN, Marcelo D.
 ; APPLICANT: TAL, Michael
 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
 ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
 ; STREET: 419 Seventh Street N.W., Ste. 300
 ; CITY: Washington

```
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-8
;
; Query Match 16.1%; Score 166.5; DB 3; Length 115;
; Best Local Similarity 27.4%; Pred. No. 1.1e-10;
; Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;
;
QY 75 CPNLWMRNGSHCYFSEMEKRDWNSLSLKFCADKGSLLTFPDNQGNLFQEVYVGEDFYWIG 134
Db 1 CSEDWVGQRCYFISTVKRSWTSQAQNCSEHGATLAVIDSEKDNWFLKRYAGREHHWG 60
;
QY 135 LRDDIG--WRWEDGPALSILSNSVQKCGTIHRCGLHASSCEVALOWICEK 185
Db 61 LKKEGHPKWSNGKEFN-NWENVGSDKCVFLKNTVSSMECEKNLYWICNK 112
;
; RESULT 13
; PCT-US95-04258-8
; Sequence 8, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
;
; Query Match 16.1%; Score 166.5; DB 3; Length 115;
; Best Local Similarity 27.4%; Pred. No. 1.1e-10;
; Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;
;
QY 75 CPNLWMRNGSHCYFSEMEKRDWNSLSLKFCADKGSLLTFPDNQGNLFQEVYVGEDFYWIG 134
Db 1 CSEDWVGQRCYFISTVKRSWTSQAQNCSEHGATLAVIDSEKDNWFLKRYAGREHHWG 60
;
QY 135 LRDDIG--WRWEDGPALSILSNSVQKCGTIHRCGLHASSCEVALOWICEK 185
Db 61 LKKEGHPKWSNGKEFN-NWENVGSDKCVFLKNTVSSMECEKNLYWICNK 112
;
; RESULT 14
; US-09-127-946-14
; Sequence 14, Application US/09127946
; Patent No. 6416973
; GENERAL INFORMATION:
; APPLICANT: Bakker, Alexander B.H.
; APPLICANT: Phillips, Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,946
; FILING DATE: 31-JUL-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/089,168
; FILING DATE: 12-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,692
; FILING DATE: 16-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,639
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/063,717
; FILING DATE: 29-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,430
; FILING DATE: 01-AUG-1997
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0763X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-127-946-14

Query Match      16.1%; Score 166.5; DB 4; Length 190;
Best Local Similarity 24.3%; Pred. No. 2.1e-10;
Matches 45; Conservative 31; Mismatches 66; Indels 43; Gaps 5;

QY 40 MVALGLLTIVL-----MSLLLYORTLCCGSGKGFMCQC----- 72
Db 5 MIISGLVVIVKVVGMTFFLLYFQVFGKSGNDGFVPTIESYGTTSVQNVSQIFGRNDESTM 64

QY 73 -----SRCPNLMWRNGSHCYFFSMKRDWNSSLKFCADKSGSHLLTFPDNQGVNLFQRYV 126
Db 65 PTRSYGTVCPRNWDPHQCKFFSFSESPWKSMDYCATQGSTLAIVNTPKLYIQDIA 124

QY 127 GEDFYWTICLRIDG---WRWEDGPALSLSILNSVVKCGTIHRCGL-----HASSCEVAL 179
Db 125 GIENYFGLVRQPGKKRWNNNSVFGNVGNVTNQDNFDCVTI---GLTKTYDAASCEVSY 181

QY 180 QWICE 184
Db 182 RWICE 186

RESULT 15
US-09-111-470-10
; Sequence 10, Application US/09111470
; Patent No. 6277959
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth E.M.
; APPLICANT: Ford, John
; APPLICANT: Saeland, Sem
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Membrane Protein Genes;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,470
; FILING DATE: 08-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,080
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0695
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-111-470-10

Query Match      15.9%; Score 164.5; DB 3; Length 273;
Best Local Similarity 27.2%; Pred. No. 5.6e-10;
Matches 34; Conservative 19; Mismatches 57; Indels 15; Gaps 3;

QY 75 CPNLMWRNGSHCYFFSMKRDWNSSLKFCADKSGSHLLTFPDNQGVNLFQRYVGEDFYWIG 134
Db 138 CPVNWVEHQDSCYWFSSHSGMSWAEAEKYCOLKNAHLVVINSRERQNFQKYLGSAYTWMG 197

QY 135 LRDIDG-WRWEDGPALSLSILNSVVK-----KCGTIHRCG-LHASSCEVAL 179
Db 198 LSDPEGAKWVDGTDYATGFQNWKPQDDQWQHGLGGGEDCAHFHDPGRWDDVCORPY 257

QY 180 QWICE 184
Db 258 HWICE 262

Search completed: August 10, 2004, 16:20:32
Job time : 15.6407 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:30:38 ; Search time 17 Seconds
(without alignments)
1069.423 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MTDSVIYMLELPTAQON.....GLQASSCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 95820

Minimum DB seq length: 0
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	2 I59421	mast cell function
2	166	16.2	156	2 T28141	C type lectin, B1
3	153.5	15.0	167	1 WMVZF2	hepatic lectin hom
4	149	14.6	170	2 T28140	natural killer cel
5	143.5	14.0	144	2 PC7027	aggratin alpha cha
6	142	13.9	146	2 JC7135	agkisacutacin beta
7	137.5	13.4	175	2 S29822	pancreatitits-assoc
8	137	13.4	165	2 A28351	pancreatic stone p
9	136	13.3	163	1 A34313	antifreeze protein
10	135	13.2	146	2 JC7105	aggratin beta chai
11	134.5	13.1	175	2 A37194	pancreatic thread
12	132.5	13.0	175	2 A41719	pancreatic stone p
13	130.5	12.8	175	2 A49616	pancreatitits-assoc
14	129.5	12.7	162	1 LNRC3	lectin BRAS-2 prec
15	128	12.5	146	2 JC4691	coagulation factor
16	128	12.5	166	1 RGHU1B	regenerating islet
17	123.5	12.1	133	2 A47267	botrocetin alpha c
18	122.5	12.0	162	1 LNRC1	lectin BRAS-1 prec
19	122	11.9	174	2 S54379	pancreatitits-assoc
20	121.5	11.9	125	2 B47267	botrocetin beta ch
21	120	11.7	123	2 JC2415	echicetin beta cha
22	119.5	11.7	131	2 JC5058	bitiscetin alpha c
23	119	11.6	129	2 JC4329	coagulation factor
24	118.5	11.6	123	2 B42972	coagulation factor
25	117	11.4	125	2 JC5059	bitiscetin beta ch
26	116	11.3	155	2 S78774	perlucin - Halioti
27	115	11.2	166	1 RGHU1A	regenerating islet
28	113	11.0	166	2 A45751	pancreatic stone p
29	111	10.9	174	2 I83377	regenerating prote

30	110.5	10.8	173	2 B47148	reg II, regenerati
31	110	10.8	165	2 A47148	reg I, regeneratin
32	108.5	10.6	152	2 JC7134	agkisacutacin alph
33	105.5	10.3	147	2 A26697	echinoidin - sea u
34	105	10.3	116	1 WMVZF8	hepatic lectin hom
35	105	10.3	152	2 JC4690	coagulation factor
36	103	10.1	174	1 A48689	pancreatitits-assoc
37	101.5	9.9	173	2 S10548	lectin - barnacle
38	100.5	9.8	142	2 S78596	ovocleidin - chick
39	100.5	9.8	168	2 F42521	A40R protein - vac
40	99.5	9.7	159	2 JQ1777	SalP2R protein pre
41	99.5	9.7	168	2 T37425	NK cell receptor h
42	99	9.7	158	2 T26692	hypothetical prote
43	95.5	9.3	147	2 JC7938	type II antifreeze
44	92.5	9.0	188	2 T33623	hypothetical prote
45	88.5	8.7	173	2 T25730	hypothetical prote

ALIGNMENTS

RESULT 1
I59421
mast cell function associated antigen - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I59421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A;Reference number: I59421; MUID:96016176; PMID:7568140
A;Accession: I59421
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <RES>
A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142
C;Genetics:
A;Gene: mafa

Query Match	51.4%;	Score	525.5;	DB	2;	Length	188;
Best Local Similarity	53.5%;	Pred. No.	4.8e-42;				
Matches	100;	Conservative	29;	Mismatches	57;	Indels	1;
Gaps	1;						
QY	1	MTDSVIYMLELPTAQONDYGPQQKSSSSKPSCLVAITLGLTAVLLSVLLQWIL	60				
Db	1	MADNSIYSTLELPAAPRVQDDSEWKYKAVLHRCVSYLVWVALGLLTVILMSLLYQTL	60				
QY	61	COGSNYSTCASCPSPDRMKVGNHCYFVSVEKDNSSLEFCLARDSHLLVITDQEMS	120				
Db	61	CCGSKGFMCSQCSRCNLMWRNGSHCIYFSMEKRDWNSSLKFCADKGSLLTTFPDQGVN	120				
QY	121	LLQVFLSEAFPCWITGLRNNSGWRWEDGSPINFSISSNFVQTGAINKNGLQASSCEVPL	180				
Db	121	LFQEVYVGDFYWITGLRIDGWRWEDGFALSLS-ILSNSVVKCGTTHRCGLHASSCEVAL	179				
QY	181	HGVCKKV	187				
Db	180	QWICEKV	186				

RESULT 2
T28141
C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
Submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAAL18961.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: Blec
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Query Match 16.2%; Score 166; DB 2; Length 156;
Best Local Similarity 29.7%; Pred. No. 2.3e-08;
Matches 46; Conservative 19; Mismatches 69; Indels 22; Gaps 5;

Qy 42 TLGLLTAVLLSVLLQWILCOGSNYSTCASCPSCDPRMKNYGNHCYFVSVEEKDWNSSLE 101
Db 6 TVLITAVAFVQAFQ-----PHEPCAQCFDWIGRGKCYFSEDESNTSSQN 56

Qy 102 FCLARDSHLLVITDQMSLLQVFLSEAFWCWIGLRNNS--GWRWEDGSPNFSRISNS 158
Db 57 NCSALGASLAVFDSAEDLSFTMRHKGSSPHWVGLSREGKEHPWVNRSP-----SHL 110

Qy 159 F-VQ---TCGAINKNGLOASSCEVPLHGVCCKVRL 189
Db 111 FVQVQDGLCAYLGDAGLSSHCSTRNWNVCTKPAL 145

RESULT 3
WMVZF2
hepatitis B virus (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])
C;Species: fowlpox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B29963
R;Tomley, F.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox virus
A;Reference number: J04442; MUID:88229622; PMID:2836548
A;Accession: B29963
A;Molecule type: DNA
A;Residues: 1-167 <TOM>
A;Cross-references: GB:D00295; NID:g221380; PID:BAA00192.1; PID:g221383
C;Superfamily: fowlpox virus hepatitis B virus
C;Keywords: early protein
F;49-152/Domain: C-type lectin homology <LCH>

Query Match 15.0%; Score 153.5; DB 1; Length 167;
Best Local Similarity 25.8%; Pred. No. 3.7e-07;
Matches 39; Conservative 29; Mismatches 74; Indels 9; Gaps 5;

Qy 36 SCLVAITLGLTAVLLSVLLQWILCOGSNYSTCASCPSCDPRMKNYGNHCYFVSVEEKD 95
Db 13 SCVAITVLGILCLILFTLVV--VTCWV-YVAFYPYFSKVCPEDEWIGYNSKCYFTINETN 69

Qy 96 WNSSLEFCLARDSHLLVITDQMSLLQVFLSEAFWCWIGLRNNSGWRWEDGSPNFSRIS 155
Db 70 WNSKKLCDVMDSSLIRPDNIETLNFVSRYGKGSY-WIDINQN---RKIPG--INFSLYY 123

Qy 156 SNSFVQTGCAINKNGLOASSCEVPLHGVCCK 186
Db 124 EQGVNDICLLFDTSNIHMSLCIFHERITCVK 154

RESULT 4
T28140
natural killer cell receptor homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28140
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: Z20475
A;Accession: T28140
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-170 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAAL18960.1
A;Experimental source: clone cB12
C;Genetics:
A;Gene: B-NK
A;Map position: 16
A;Note: Intron positions not resolved (incomplete sequence)

Query Match 14.6%; Score 149; DB 2; Length 170;
Best Local Similarity 28.6%; Pred. No. 9.9e-07;
Matches 34; Conservative 16; Mismatches 67; Indels 2; Gaps 2;

Qy 70 ASCPSCDPRMKNYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEA 129
Db 45 AACLCHQFVWLLGDRCYELSTEGKNWTQAKKCNLSQSLAVLRKKAEEHDLQOMAGAE 104

Qy 130 FCWIGLR-NNSGWRWEDGSPNFSRISNSFVQT-CGAINKNGLOASSCEVPLHGVCCK 186
Db 105 FVMIGLEVSTNQMKWDNSSYNSTESDNLVSMENRCGTFKNTKVEGDVCSGHEQWVCOK 163

RESULT 5
PC7027
aggritin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggritin, a collagen-like platelet
A;Reference number: PC7027; MUID:59443731; PMID:10512747
A;Accession: PC7027
A;Molecule type: mRNA
A;Residues: 1-144 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom

Query Match 14.0%; Score 143.5; DB 2; Length 144;
Best Local Similarity 29.6%; Pred. No. 2.7e-06;
Matches 34; Conservative 17; Mismatches 49; Indels 15; Gaps 4;

Qy 68 TCASCPCDPRMKNYGNHCYFVSVEEKDWNSSLEFCLARD--SHLLVITDQMSLLQVF 125
Db 6 TRAGLEDCDFGWSFYDQHCYQAFNEQKTWDEAEKFCRAQENGHAHASTESNGEADFVSWL 65

Qy 126 LS-----EAFCWIGLR-----NNSGWRWEDGSPNFSRISNSFVQTGCAINK 168
Db 66 ISQKDELADEYVWIGLRQAKNQKQCSSEWSGSSVSYENL-IDLHTKKCGALEK 119

RESULT 6
JC7135
agkiscatutacin beta chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic veno
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7135
A;Molecule type: mRNA
A;Residues: 1-146 <CHE>
A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-146/Product: egkiascutacin beta chain #status experimental <MAT>

Query Match 13.9%; Score 142; DB 2; Length 146;
Best Local Similarity 25.0%; Pred. No. 3.9e-06;
Matches 42; Conservative 21; Mismatches 55; Indels 50; Gaps 8;

QY 39 VAITGLLAVLLVLLVYLWILCOGNSYTCASCPCPRRMKYNHCYFVSVEKDWN 98

Db 5 IFVSGLLVVFL-----SLSGFAADCPSEWSSYEGHCYKPFDEPKTWAD 48

QY 99 SLEFCLAA--RDShLLVITDNOE-----MSLLQVFLSEAFQWIGLR---NNSGMRWEDGSP 149

Db 49 AEKFCQKHGSHLAFHSSEADFVTLTPSLKTDVLWIGLKNWGCYKWSGDKL 108

QY 150 NF-----SRISNSFV--QTCAINKNGLQASCEVPLHGVC 185

Db 109 DYKDMREQECLVSRVTNNWLSMDCG-----TTCSEF-----VCK 143

RESULT 7

S29822

pancreatitis-associated protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

C:Accession: S29822

R:Ittoh, T.; Teraoka, H.

Biochim. Biophys. Acta 1172, 184-186, 1993

A:Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homolog

A:Reference number: S29821; MUID:93176807; PMID:7679928

A:Accession: S29822

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-175 <I>O>

A:CROSS-references: GB:D13509; NID:g286106; PIDN:BAA02727.1; PID:g286107

C:Superfamily: tetranectin; C-type lectin homology

F;40-171/Domain: C-type lectin homology <LCH>

Query Match 13.4%; Score 137.5; DB 2; Length 175;

Best Local Similarity 25.7%; Pred. No. 1.2e-05;

Matches 46; Conservative 28; Mismatches 70; Indels 35; Gaps 9;

QY 33 PSCSLVAITLGLTAVLLVLLVYLWILCOGNSYTCASCPC---SCEDRMKYNHCY 88

Db 3 PPTACSV-----MSWLLSLCLM---LLSQVQEDSLKNIPSAISCPKGSQAYGICYA 53

QY 89 FSVEEKDWNSSLEFCLAR--DSHLLVITDNOEMLLQVFL-----SFAFCWIGLR----- 136

Db 54 LFIQIPQTFDAELACQKRPQGHVLSVLSAEASFSLSMVKRTGNSYQYTWIGLHDPTLGA 113

QY 137 --NNSGMRWEDGSPLEFNSRISNSFVQT-----CGAINK--NGL---QASCEVPLHGVC 185

Db 114 BPNGGWEWSNNDVMYFNWERNPSTALDRAFCGLSRASGFLKWRDTCVKLPYVCK 172

RESULT 8

A28351

pancreatic stone protein precursor - rat

N:Alternate names: lithostathine

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-May-2000

C:Accession: A28351; A39081; PL0147; S34618

R:Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto

J. Biol. Chem. 263, 2111-2114, 1988

A:Title: A novel gene activated in regenerating islets.

A:Reference number: A92704; MUID:88115343; PMID:2963000

A:Accession: A28351

A:Molecule type: mRNA

A:Residues: 1-165 <TER>

A:CROSS-references: GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605

R:Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagorn, J.C.; Giorgi, D.

J. Biol. Chem. 266, 786-791, 1991

A:Title: Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine

A:Reference number: A39081; MUID:91033273; PMID:1985964

A:Accession: A39081

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-165 <ROU>

A:CROSS-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463

R:Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovey, M.

Comp. Biochem. Physiol. B 93, 793-797, 1989

A:Title: Characterization in rat pancreatic juice of a protein homologous to the human I

A:Reference number: PL0147; MUID:90031455; PMID:2680252

A:Accession: PL0147

A:Molecule type: protein

A:Residues: 22-69 <ADR>

A:Experimental source: pancreas

R:Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.

Biochim. Biophys. Acta 1174, 99-102, 1993

A:Title: Rapid PCR cloning and sequence determination of the rat lithostathine gene.

A:Reference number: S34618; MUID:93326645; PMID:7916640

A:Accession: S34618

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <DUS>

A:CROSS-references: EMBL:L07512; NID:g393208; PIDN:AAA41533.1; PID:g393209

C:Comment: This protein is found in pancreatic calculi of mammals. A peptide bond between

rocin into an insoluble protein at a neutral pH of 5.5 to 7.5.

C:Genetics: 21/1; 60/3; 106/3; 144/1

C:Superfamily: tetranectin; C-type lectin homology

C:Keywords: pyrrolidone acid

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-165/Product: pancreatic stone protein #status predicted <MAT>

F;35-161/Domain: C-type lectin homology <LCH>

F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer

Query Match 13.4%; Score 137; DB 2; Length 165;

Best Local Similarity 27.2%; Pred. No. 1.3e-05;

Matches 43; Conservative 23; Mismatches 68; Indels 24; Gaps 7;

QY 49 VLLSVLLVYLWILCOGNSYTCASCPC---CDPRMKYNHCYFVSVEKDWNSSLEFCL 104

Db 8 ILLSLCLM---VLSPSQGEAEEDLPSARITCEGNSAYSSCYFYFMEHLWSAEADLFCQ 64

QY 105 ARDS--HLLVITDNOEMLLQVFLSE-----AFWIGL---RNSGMRWEDGSPLEF 151

Db 65 NNSGVLVSVLSQAEQNFSLATIKSGTTAAVNVWIGLHDPKNNRRWHWSGSLFLYKSWD 124

QY 152 SRISNSFVQTCAINKNG---LQASCEVPLHGVC 185

Db 125 TGYPNNSNGYCVSVTSNSGYKKWRDNSCDALQSLFVCK 162

RESULT 9

A34313

antifreeze protein II precursor - sea raven

N:Alternate names: pro-antifreeze protein type II

C:Species: Hemiripiterus americanus (sea raven)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A34313; A24602; PC2386; PC2387; S65733

R:Hayes, P.H.; Scott, G.K.; Ng, N.F.L.; Hew, C.L.; Davies, P.L.

J. Biol. Chem. 264, 18761-18767, 1989

A:Title: Cystine-rich type II antifreeze protein precursor is initiated from the third .

A:Reference number: A34313; MUID:90036986; PMID:2572595

A:Accession: A34313

A:Molecule type: DNA; mRNA

A:Residues: 1-37, 'G', 39-163 <HAY>

A:CROSS-references: GB:J05100; NID:g213875; PIDN:AAA49618.1; PID:g213876

A>Note: there are 12-15 copies in the genome; the sequence of SR7 was determined

A>Note: the initiator codon was determined

A>Note: parts of this sequence, including the amino end of the mature protein, were det

A>Note: the amino end of the mature protein is blocked

R:Ng, N.F.; Trinh, K.Y.; Hew, C.L.

J. Biol. Chem. 261, 15690-15695, 1986

A:Title: Structure of an antifreeze polypeptide precursor from the sea raven, Hemiripit

A:Reference number: A24602; MUID:87057207; PMID:3782083

A;Reference number: A59313
A;Accession: A59313
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-175 <DUS2>
A;Cross-references: GB:107127; NID:G349550; PIDN:AAA41805.1; PID:G349551
A;Note: an incorrect initiation codon was used
R;Iovanna, J.L.; Keim, V.; Boeshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dagorn
Am J. Physiol. 265, G611-G618, 1993
A;Title: FAP, a pancreatic secretory protein induced during acute pancreatitis, is expressed in the rat pancreas
A;Reference number: I51899; MUID:94056762; PMID:8238345
A;Accession: I51899
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-175 <IOV1>
A;Cross-references: GB:M98049; NID:G393210; PIDN:AAA16341.1; PID:G393211
A;Note: in Genbank entry R4PAPC, release 113.0, the source is designated as Rattus rattus
R;Kaminura, T.; West, C.; Reutler, E.
Gene 118, 299-300, 1992
A;Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
A;Reference number: JCI257; MUID:92380521; PMID:1511905
A;Accession: JCI257
A;Molecule type: mRNA
A;Residues: 1-6, 'S', '8-175 <KAM>
A;Cross-references: GB:S43715; NID:G254694; PIDN:AA23103.1; PID:G254695
R;Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
J. Biol. Chem. 266, 24664-24669, 1991
A;Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a novel protein
A;Reference number: A41719; MUID:92105133; PMID:1722211
A;Accession: A41719
A;Molecule type: mRNA
A;Residues: 1-175 <IOV2>
A;Cross-references: GB:M55149; NID:G206030; PIDN:AAA41807.1; PID:G206031
A;Note: the amino-terminal residue of the mature protein was identified as Glu
C;Genetics:
A;Gene: pap
A;Introns: 26/1; 65/3; 111/3; 154/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: lectin; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match 13.0%; Score 132.5; DB 2; Length 175;
Best Local Similarity 25.4%; Pred. No. 3.6e-05;
Matches 42; Conservative 28; Mismatches 68; Indels 29; Gaps 7;
QY 45 LLTAVLLVLLYQWILCOGSNYSTCASC-----SCPDRWKYGNHCYFVSVEKDWNSL 100
Db 9 VMSWMLLSCLM---LISVQGESEPKIPSPARISCPKSGQAYGVCYALPQIPCTWFDAAE 65
QY 101 EFCILAR-DSHLVITDNOEMLLQVFL-----SEAFCWIGLR-----NNSGWRWEDG 146
Db 66 LAQKPEGHVSLVNAEASFSLAMVKNYQYQVYTWICLHDPTLGGRNGGGSNSN 125
QY 147 SPINFRISNSVQVT-----CGAINKNG-----IQASCEVPLHGVCCK 185
Db 126 DIMNYVWERNPSTALDRGFCGSLRSGFLRWDRDTCVKLPYVCK 172

RESULT 13
A49616
pancreatitis-associated protein precursor - human
N;Alternate names: C-type lectin; pancreatic human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000
C;Accession: A49616; A44931; S29821; S48197; I55580
R;Dusetti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
Genomics 19, 108-114, 1994
A;Title: Molecular cloning, genomic organization, and chromosomal localization of the human BRA3-2 precursor - barnacle (Megabalanus rosa)
A;Reference number: A49616; MUID:94245143; PMID:8188210

A;Accession: A49616
A;Molecule type: DNA
A;Residues: 1-175 <DUS>
A;Cross-references: GB:DL15533; NID:G482308; PIDN:AAA60020.1; PID:G482909
R;Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C.
Cancer Res. 52, 5089-5095, 1992
A;Title: A novel gene (HIP) activated in human primary liver cancer.
A;Reference number: A44931; MUID:92386513; PMID:1325291
A;Accession: A44931
A;Molecule type: mRNA
A;Residues: 1-175 <LAS>
A;Cross-references: GB:X68641; NID:G312806; PIDN:CAA48605.1; PID:G312807
A;Experimental source: hepatocellular carcinoma
A;Note: sequence extracted from NCBI backbone (NCBIN:113007, NCBIP:113008)
R;Itoh, T.; Teraoka, H.
Biochim. Biophys. Acta 1172, 184-186, 1993
A;Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homologs of the rat Reg-2 protein
A;Reference number: S29821; MUID:93176807; PMID:7679928
A;Accession: S29821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-175 <ITO>
A;Cross-references: GB:DL13510; NID:G285970; PIDN:BAA02728.1; PID:G285971
R;Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Vernier, P.
Eur. J. Biochem. 224, 29-38, 1994
A;Title: Structural organization and chromosomal localization of a human gene (HIP/PAP)
A;Reference number: S48197; MUID:94357229; PMID:8076648
A;Accession: S48197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-175 <LA2>
R;Orelle, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
J. Clin. Invest. 90, 2284-2291, 1992
A;Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in transgenic mice
A;Reference number: I55580; MUID:93107309; PMID:1469087
A;Accession: I55580
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-175 <RES>
A;Cross-references: GB:S51768; NID:G262368; PIDN:AA24642.1; PID:G262369
C;Genetics:
A;Gene: GDB:PAP; HIP
A;Cross-references: GDB:136839; OMIM:167805
A;Map position: 2p12-2p12
A;Introns: 26/1; 65/3; 111/3; 154/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: acute phase; extracellular protein; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status predicted <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match 12.8%; Score 130.5; DB 2; Length 175;
Best Local Similarity 26.0%; Pred. No. 5.6e-05;
Matches 46; Conservative 25; Mismatches 71; Indels 35; Gaps 8;
QY 38 LVAITGLTAVLLSVLLYQWILCOGSNYSTCASCPS-----CPDRWKYGNHCYFVSVEE 93
Db 2 LPPMALPSVSWMLLSCLM---LISVQGESEPKIPSPARISCPKSGKAYGVCYALFLSP 58
QY 94 KDNWSSLEFCLARDS-HLLVITDNOEMLLQVFL-----SEAFCWIGLR-----NNS 139
Db 59 KSWTDADLACQRRPNSGNLVSILSGAEGSFVSLVSKISGNSYSYVWTLGLHDPTGGTFPGE 118
QY 140 GWRWEDGSPINL-----SRISNSFVQTCAINKNGL-----QASSCVPLHGVCCK 185
Db 119 GMEWSSDDVMYFAWERNFTISSPGH---CASLSRSTAFLEWKDYNVRLPYVCK 172

RESULT 14
LNRC3
lectin BRA3-2 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:20:38 ; Search time 13 Seconds

(without alignments)
757.020 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 WTDSVIYSMLPLTATQON.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 41282

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198.5	19.4	179	1 CD94 MACMU	Q9mzk9 macaca mula
2	196.5	19.2	179	1 CD94 HUMAN	Q1241 homo sapien
3	194.5	19.0	179	1 CD94 PANTR	Q9mz41 pan troglod
4	175	17.1	149	1 CLE2 HUMAN	Q92478 homo sapien
5	156.5	15.3	163	1 V239 FOWPV	Fl4371 fowlpox vir
6	153.5	15.0	167	1 V008 FOWPV	Pl4370 fowlpox vir
7	147.5	14.4	175	1 PBCG MESAU	Q92778 mesocricetu
8	147	14.4	174	1 PAP3 MOUSE	O09049 mus musculu
9	146	14.3	117	1 CHBB CROHO	P81509 crotalus ho
10	137.5	13.4	175	1 PAP1 MOUSE	P35230 mus musculu
11	137	13.4	165	1 LITH RAT	Fl0758 rattus norv
12	136	13.3	163	1 ANP HEMAM	P05140 hemitriptier
13	134.5	13.1	175	1 LITH BOVIN	P23132 bos taurus
14	134.5	13.1	175	1 PAP2 MOUSE	O09037 mus musculu
15	134	13.1	146	1 MMHB AGKHA	O9yi92 agkistrodon
16	132.5	13.0	175	1 PAP1 RAT	P25031 rattus norv
17	132	12.9	148	1 CVXB CRODU	O93427 crotalus du
18	130.5	12.8	175	1 PAP1 HUMAN	O06141 homo sapien
19	129.5	12.7	162	1 LEC3 MEGRO	P07439 megabalanus
20	128	12.5	146	1 IXB TRIFL	P23807 trimeresuru
21	128	12.5	166	1 LITB HUMAN	P48304 homo sapien
22	126	12.3	133	1 RHCA AGKRH	P81397 agkistrodon
23	124	12.1	123	1 ABAA TRIAB	P81114 trimeresuru
24	123.5	12.1	133	1 BOTA BOTJA	P22029 bothrops ja
25	123	12.0	131	1 ABAL TRIAB	P81111 trimeresuru
26	123	12.0	155	1 PLC HALLA	P82596 halictis la
27	123	12.0	158	1 CVXA CRODU	O93426 crotalus du
28	122	11.9	174	1 PAP3 RAT	P42854 rattus norv
29	121.5	11.9	125	1 BOTB BOTJA	P22030 bothrops ja
30	120	11.7	123	1 ECHB ECHCA	P81996 echis carin
31	115	11.2	134	1 ABAA TRIAB	P81112 trimeresuru
32	115	11.2	166	1 LITA HUMAN	P05451 homo sapien
33	113.5	11.1	158	1 NKGF PANTR	Q95mil pan troglod

RESULT 1

ID	CD94_MACMU	STANDARD;	PRT;	179 AA.
AC	Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Natural killer cells antigen CD94 (NK cell receptor) (Killer cell			
DE	lectin-like receptor subfamily D, member 1).			
GN	KLRD1 OR CD94.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;			
OC	Cercopitheciinae; Macaca.			
OX	NCBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).			
RX	MEDLINE=20322487; PubMed=10866118;			
RA	LaBonte M.L., Levy D.B., Letvin N.L.;			
RT	"Characterization of rhesus monkey CD94/NKG2 family members and			
RT	identification of novel transmembrane-deleted forms of NKG2-A, B, C,			
RT	and D.";			
RL	Immunogenetics 51:496-499(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=21158386; PubMed=11261935;			
RA	Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;			
RT	"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative			
RT	splicing of 5' exons in rhesus monkey decidua.";			
RL	Immunogenetics 53:69-73(2001).			
CC	-!- FUNCTION: Plays a role as a receptor for the recognition of MHC			
CC	class I HLA-E molecules by NK cells and some cytotoxic T-cells.			
CC	-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family			
CC	members.			
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=1; Synonyms=CD94-A;			
CC	isoId=Q9MZK9-1; Sequence=Displayed;			
CC	Name=2; Synonyms=CD94-B;			
CC	isoId=Q9MZK9-2; Sequence=VSP_003055;			
CC	Name=3; Synonyms=CD94 alt;			
CC	isoId=Q9MZK9-3; Sequence=VSP_003054;			
CC	-!- TISSUE SPECIFICITY: Natural killer cells.			
CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF190931; AAF74527.1; --			
DR	EMBL; AF190932; AAF74528.1; --			

ALIGNMENTS

34	113	11.0	125	1	ABA3 TRIAB
35	112.5	11.0	122	1	LITH_PIG
36	111.5	10.9	132	1	ABBA TRIAB
37	110.5	10.8	173	1	LIT2 MOUSE
38	110	10.8	165	1	LIT1 MOUSE
39	109	10.7	157	1	MMHA AGKHA
40	106.5	10.4	158	1	NKGF_HUMAN
41	105.5	10.3	147	1	LECE_ANTCR
42	105	10.3	152	1	IXA_TRIFL
43	103	10.1	174	1	PAP2 RAT
44	100.5	9.8	142	1	OC17 CHICK
45	100.5	9.8	168	1	VA40_VACCC

P81113	trimeresuru
Q29191	sus scrofa
P81115	trimeresuru
Q08731	mus musculus
P43137	mus musculus
Q9Y959	agkistrodon
O43308	homo sapien
P06027	anthocidari
P23806	trimeresuru
P35231	rattus norv
Q9PR58	gallus gall
P21063	vaccinia vi

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DR EMBL; AF190933; AAF74529.1; -.
DR EMBL; AF294886; AAG34498.1; -.
DR HSP; P22897; LEGG.
DR InterPro; IPR001304; Lectin C.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS00411; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 132 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 1 34 MAVKFTLRLISGTLGIICLSLWATLGLKNS -> MAA
(in isoform 3).
FT FTid=VSP_003054.
FT L -> LQ (in isoform 2).
FT FTid=VSP_003055.
FT Y -> D.
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SQ SEQUENCE 179 AA; 20607 MW; 06212B494527F07 CRC64;

Query Match 19.4%; Score 198.5; DB 1; Length 179;
Best Local Similarity 33.3%; Pred. No. 5.6e-12;
Matches 54; Conservative 24; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSLVAITLGLTAVLLSVLLYOWILCOGSN--YSTCASCPSPDRMKNYCHCVTSVE 92
DB 20 CLSLMA-TLGLLLKNSFKLSVEPAYTPGNIEIQKSDCCSCHEKMGVPCNCFISSE 78
QY 93 EKWNSSLEFCIARDSHLLVITDQEMSLQVFLSEAFCTWGL---RNNSGRWEDGSPL 149
DB 79 EKTWNESRHFCAQSKSSLLQNRDELDFMS--SSQHFYWLGLSVSEHTAWLWENGSA 136
QY 150 NFSRISNSP-----VQTGAINKNG-LOASCEVPLHGVCKK 186
DB 137 --SQYLFPSFTFPKNCIAYNSKGNALDESCETKNRYICKQ 176

RESULT 2
CD94_HUMAN
ID CD94_HUMAN STANDARD; PRT; 179 AA.
AC Q13241; Q43321; Q43773; Q9UBB3; Q9UEQ0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
leutin-like receptor subfamily D, member 1) (KP43).
GN KLRD1 OR CD94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=96011848; PubMed=7589107;
RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
RA Lanier L.L.;
RT "Molecular characterization of human CD94: a type II membrane
glycoprotein related to the C-type lectin superfamily.";
RL Eur. J. Immunol. 25:2433-2437(1995).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98139529; PubMed=9472066;
RA Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,

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RA Lebrach H., Francis P., Lopez-Botet M.;
RT "Structure of the human CD94 C-Type lectin gene.";
RL Immunogenetics 47:305-309(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Biassoni R.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=98267245; PubMed=9601951;
RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,
RA Tohma S., Inoue T., Yamamoto K., Juji T.;
RT "A alternatively spliced form of the human CD94 gene.";
RN Immunogenetics 48:87-88(1998).
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RP SEQUENCE FROM N.A. (ISOFORM 1).
RN TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.B.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
IsoId=Q13241-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q13241-2; Sequence=VSP_003053;
Name=3; Synonyms=CD94 alt;
IsoId=Q13241-3; Sequence=VSP_003052;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm".
-----
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EMBL; U30610; AAC50291.1; -.
DR EMBL; Y14287; CAA74663.1; -.
DR EMBL; Y14288; CAA74663.1; JOINED.
DR EMBL; AJ000673; CAA04230.1; -.
DR EMBL; AJ000001; CAA03845.1; -.
DR EMBL; AB009597; BAA24450.1; -.
DR EMBL; AB010084; BAA24451.1; -.
DR EMBL; BC028009; AAH28009.1; -.
DR PDB; 1B6E; 15-JUN-99.

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DR Genew: HGNC:6378; KLRD1.
DR MIM: 602894; -.
DR GO: GO:0005886; C:plasma membrane; TAS.
DR GO: GO:0004888; P:transmembrane receptor activity; TAS.
DR GO: GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE: PS00041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing; 3D-structure.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 34 MAVFTTLWRLISGTLGIICLSIMATLIGLLKNS -> MAA
(in isoform 3).
FT VARSPLIC 105 105 /FTId=VSP 003052.
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT VARSPLIC 105 105 /FTId=VSP 003053.
SQ SEQUENCE 179 AA; 20497 MW; 1884D99E8D9583A7 CRC64;
Query Match 19.2%; Score 196.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 8.6e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCLVAITLGLTAVLLSVLLYQWILLCOGSN--YSTCASCPCPCDPRMVKYGNHCYFVSVE 92
DB 20 CLSLMA-TLIGLLKNSFTKLSIEPFTPGNLELQKSDCCSCQKWKVGRNCYFISSE 78
QY 93 EKDWSSLEFCLARDSHLIVITDQEMSLQLQVLFSEAFQWIGL---RNSGWRWEDGSPL 149
DB 79 QKTWESRHLCASQKSSLLQQLQNTDELDFMS--SSQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFRSISNSF----VQTCGAINKG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDEKKNRYICKQ 176
RESULT 3
CD94_PANTR
ID_CD94_PANTR STANDARD; PRT; 179 AA.
AC Q9MZ41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1).
GN KLRD1 OR CD94.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]_TaxID=9598;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20350666; PubMed=10994168;
RA Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
RA Muir D.G., Canavez F., Cooper S.L., Valiente N.M., Lanier L.L.,
RA Parham P.;
RT "rapid evolution of NK cell receptor systems demonstrated by
comparison of chimpanzees and humans."
RL Immunity 12:687-698 (2000).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=21623889; PubMed=11751968;
```

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RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,
RA Cleland S., Guethlein L.A., Uhrberg M., Parham P.;
RT "Conservation and variation in human and common chimpanzee CD94 and
NK2 genes."
RL J. Immunol. 168:240-252 (2002).
CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC
class I HLA-E molecules by NK cells and some cytotoxic T-cells.
CC -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
members.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms seem to exist;
CC Name=1; Synonyms=CD94-A;
CC IsoId=Q9MZ41-1; Sequences=Displayed;
CC Name=2; Synonyms=CD94-B;
CC IsoId=Q9MZ41-2; Sequences=VSP 003056;
CC -!- TISSUE SPECIFICITY: Natural killer cells.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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DR EMBL: AF259054; AAF86964.1; -.
DR HSSP: P22897; 1EGG.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE: PS00041; C-TYPE LECTIN 2; 1.
KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;
KW Alternative splicing.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).
FT DISULFID 61 72 BY SIMILARITY.
FT DISULFID 89 174 BY SIMILARITY.
FT DISULFID 152 166 BY SIMILARITY.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 105 105 L -> LQ (in isoform 2).
FT VARSPLIC 105 105 /FTId=VSP 003056.
SQ SEQUENCE 179 AA; 20493 MW; 7244D99E8D9587E7 CRC64;
Query Match 19.0%; Score 194.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 1.3e-11;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCLVAITLGLTAVLLSVLLYQWILLCOGSN--YSTCASCPCPCDPRMVKYGNHCYFVSVE 92
DB 20 CLSLMA-TLIGLLKNSFTKLSIEPFTPGNLELQKSDCCSCQKWKVGRNCYFISSE 78
QY 93 EKDWSSLEFCLARDSHLIVITDQEMSLQLQVLFSEAFQWIGL---RNSGWRWEDGSPL 149
DB 79 QKTWESRHLCASQKSSLLQQLQNTDELDFMS--SSQFYWIGLSYSEHTAWLWENGSA 136
QY 150 NFRSISNSF----VQTCGAINKG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDEKKNRYICKQ 176
RESULT 4
CLE2_HUMAN
ID_CLE2_HUMAN STANDARD; PRT; 149 AA.
AC Q92478; Q9UBQ4;
DT 28-FEB-2003 (Rel. 41, Created)
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DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW SIGNAL; LECTIN.
FT CHAIN 1 26 BY SIMILARITY.
FT DOMAIN 27 175 PANCREATIC BETA CELL GROWTH FACTOR.
FT DISULFID 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19940 MW; 3854F36BA35D17CE CRC64;

Query Match 14.4%; Score 147.5; DB 1; Length 175;
Best Local Similarity 24.6%; Pred. No. 4.1e-07;
Matches 42; Conservative 34; Mismatches 72; Indels 23; Gaps 7;

QY 38 LVAITLGLLTAVALLS-VLLYQWILCOGSNYSTCSCPCSPDRWKKYGNHCYFVSVEKDW 96
Db 2 MLPMLCRMSWMLLSCLMLLSQVGEVAKKADAPSSRSSCPKGSRAVGYCYVALFSVSKNW 61
QY 97 -NSSLEFCLARDSHLLVITDQEMSLLOVFLSEA-----FCWIGLR-----NNSGWR 142
Db 62 SNAELSCQMHPFSGHLAFLITSTGEITFVSSLVKNSLITAYQYIWIIGHDPHSGHTLNGSGWK 121
QY 143 WEDGSPINFSRISNSFVQT-----CGAIN-KXGLQA-----SCSEVPLHGVCVK 185
Db 122 WSSSNVLTFTYWNERNPSIAADRGYCAVLSSQSGFQKWRDFNCENELPYICK 172

RESULT 8
PAP3 MOUSE
ID PAP3_MOUSE STANDARD; PRT; 174 AA.
AC 009049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pancreaticis-associated protein 3 precursor (REG III-gamma).
OS PAP3 OR REG3G.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas;
RX MEDLINE=97208868; PubMed=9055810;
RA Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL Gene 185:159-168(1997).
CC -!- FUNCTION: Might be a stress protein involved in the control of
CC bacterial proliferation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Constitutively expressed in the small
CC intestine, moderately in colon and at an extremely low level in
CC healthy pancreas.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D63361; BAA18930.1; -.
CC DR EMBL; D63362; BAA18931.1; -.
CC DR HSSP; P05451; 111T.
CC DR MGD; MGI:109406; Reg3g.
CC DR InterPro; IPR001304; Lectin C.
CC DR InterPro; IPR003990; Pancreatis_ac.
CC Pfam; PF00059; lectin_c; 1.

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DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW SIGNAL; LECTIN; Inflammatory response; Acute phase; Multigene family.
FT CHAIN 1 26 PANCREATITIS-ASSOCIATED PROTEIN 3.
FT DOMAIN 27 174 C-TYPE LECTIN (LONG FORM).
FT DISULFID 38 172 BY SIMILARITY.
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 170 BY SIMILARITY.
FT DISULFID 145 162 BY SIMILARITY.
SQ SEQUENCE 174 AA; 19307 MW; 5575B9E56A4D8CEF CRC64;

Query Match 14.4%; Score 147; DB 1; Length 174;
Best Local Similarity 26.5%; Pred. No. 4.5e-07;
Matches 45; Conservative 30; Mismatches 73; Indels 22; Gaps 7;

QY 38 LVAITLGLLTAVALLS-VLLYQWILCOGSNYSTCSCPCSPDRWKKYGNHCYFVSVEKDW 96
Db 2 LPRITITMSWMLLSCLMLLSQVGEVAKKADAPSSRSSCPKGSRAVGYCYVALFSVSKNW 61
QY 97 NSSLEFCLARDS-HLLVITDQEMSLLOVFL-----SEAFWIGLR-----NNSGWR 142
Db 62 YDADMACQKRPSPGHLVSVLSGAEASFLSSMIKSSGSGQYVWIGLHDPHTLGYEPNRGWE 121
QY 143 WEDGSPINFSRISNSN---SFVQTGAINK-NGL---OASSCEVPLHGVCVK 185
Db 122 WSNADVWNYINWEINPSSSSNGHCGTLRSAGFLKWRNYCNLELPYVCK 171

RESULT 9
CHBB CROHO
ID CHBB_CROHO STANDARD; PRT; 117 AA.
AC P81503;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CHB-B beta subunit.
OS Crotalus horridus horridus (Timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=8823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton alboaggregin from Trimeresurus
RT albolabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -!- FUNCTION: Binds to platelet GpIb/IX receptor system, inhibits VWF
CC binding, and stimulates agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00156; ANTIPEEEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 9 116 C-TYPE LECTIN.
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 115 BY SIMILARITY.
FT DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
FT DISULFID 95 107 (POTENTIAL).
FT DISULFID 95 107 BY SIMILARITY.

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SQ SEQUENCE 117 AA; 13888 MW; 07835BBCB61E9EAD CRC64;

Query Match 14.3%; Score 146; DB 1; Length 117;
Best Local Similarity 28.4%; Pred. No. 3.6e-07;
Matches 33; Conservative 20; Mismatches 57; Indels 6; Gaps 3;

QY 75 CPDRWMKYGNHCYFVSVEEKDWNSSLEFCLARD--HLLVITDQMSLLQVLSFAFCW 132
DQ 2 CPDWSYEGHCYRVFQEQMTWDAKFCQQHTGHLVFSFRSEEVDFVLSLKFDLFW 61
QY 133 IGLR---NNSGWRWEDGSPNFRISNSFVQTCGAINKGLQASSCEVPLHGVCV 185
DQ 62 MGRDITWNERRLQWSDTKVNYKAWGAEPICVCRATDNCQL-STSCSKTHNVVCK 116

RESULT 10
PAP1_MOUSE
ID PAP1_MOUSE STANDARD; PRT; 175 AA.
AC P35230;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (REG III-beta).
GN PAP OR PAP1 OR REG3B.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Pancreas, and Small intestine;
RX MEDLINE=93176807; PubMed=7679928;
RA Itoh T., Teraoka H.;
RT "Cloning and tissue-specific expression of cDNAs for the human and
RT mouse homologues of rat pancreatitis-associated protein (PAP).";
RL Biochim. Biophys. Acta 1172:184-186(1993).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=97208866; PubMed=9055810;
RA Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegII alpha, RegIII beta, RegIII gamma.";
RL Gene 185:159-168(1997).
CC -!- FUNCTION: Might be a stress protein involved in the control of
CC bacterial proliferation.
CC -!- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
CC PANCREATIC ACINAR CELLS (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: Constitutively expressed in the small
CC intestine, moderately in colon and at an extremely low level in
CC healthy pancreas.
CC -!- INDUCTION: Appears in pancreatic juice after induction of
CC pancreatic inflammation.
CC -!- DISEASE: Overexpressed during the acute phase of pancreatitis.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; D13509; BAA02727.1; -
DR EMBL; D63359; BAA18928.1; -
DR EMBL; D63360; BAA18929.1; -
DR FIR; S29822; S29822.
DR HSSP; P05451; 1LIT.
DR MGD; MGI:97478; Pap.
DR InterPro; IPR001304; Lectin_C.
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DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Signal; Lectin; Inflammatory response; Acute phase; Multigene family.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19476 MW; 44B3101171E79775 CRC64;

Query Match 13.4%; Score 137.5; DB 1; Length 175;
Best Local Similarity 25.7%; Pred. No. 3.7e-06;
Matches 46; Conservative 28; Mismatches 70; Indels 35; Gaps 9;

QY 33 PSCSLVAITLGLLFAVLISLVLYQWILCOGNSYTCASCP----SCPDRWMKYGNHCY 89
DQ 3 PPTACSV-----MSWMLLSCLM--LLSQVQGEDSLKNIPSAISCPKGSQAYGSYCYA 53
QY 89 FSVEEKDWNSSLEFCLAR--DSHLLVITDQMSLLQVFL-----SEAFWIGLR----- 136
DQ 54 LFIQIPQTFDAELACQKRGFGLVSVLSNAEASFSSVMYKRTGNSYQYTWIGLHDPFLGA 113
QY 137 --NNSGWRWEDGSPNFRISNSFVQTCGAINK-NGL---QASSCEVPLHGVCV 185
DQ 114 EPNGGGSWNSNDVMYFNWERNPFTALDRAFGSLSRASGLKWDMTCEVKLPVCK 172

RESULT 11
LITH RAT
ID LITH RAT STANDARD; PRT; 165 AA.
AC P10758;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic
DE thread protein) (PTP) (Islet of langerhans regenerating protein) (REG)
DE (Islet cells regeneration factor) (ICRF).
GN REG1 OR REG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91093273; PubMed=1985964;
RA Rouquier S., Verdier J.M., Iovanna J., Dagorn J.-C., Giorgi D.;
RT "Rat pancreatic stone protein messenger RNA. Abundant expression in
RT mature exocrine cells, regulation by food content, and sequence
RT identity with the endocrine reg transcript.";
RL J. Biol. Chem. 266:786-791(1991).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=88115343; PubMed=2963000;
RA Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,
RA Tochino Y., Okamoto H.;
RT "A novel gene activated in regenerating islets.";
RL J. Biol. Chem. 263:2111-2114(1988).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=93326645; PubMed=7916640;
RA Dusetti N.J., Frigerio J.M., Dagorn J.-C., Iovanna J.L.;
RT "Rapid PCR cloning and sequence determination of the rat
RT lithostathine gene.";
RL Biochim. Biophys. Acta 1174:99-102(1993).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA Miyashita H., Suzuki Y., Watanabe T., Unno M., Moriizumi S.,
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RA Yonekura H., Okamoto H.;
RT "Structure and characterization of rat Reg I gene.";
RL Seikagaku 65:1082-1082(1993).
RN [5]
RP SEQUENCE OF 22-69.
RC TISSUE=Pancreas;
RX MEDLINE=90031455; PubMed=2680252;
RA Adrich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., Rovey M.;
RT "Characterization in rat pancreatic juice of a protein homologous to
RL the human pancreatic stone protein.";
RL Comp. Biochem. Physiol. 93B:793-797(1989).
CC -!- FUNCTION: Might act as an inhibitor of spontaneous calcium
CC carbonate precipitation.
CC -!- TISSUE SPECIFICITY: Expressed only in regenerating islets, but
CC not in normal pancreatic islets, insulinomas or regenerating
CC liver.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; L07512; AAA41533.1; -
DR EMBL; M62930; AAA41974.1; -
DR EMBL; M18962; AAA42028.1; -
DR EMBL; D26164; BAA05149.1; -
DR PIR; A28351; A28351.
DR HSP; P05451; ILIT.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR01504; PNCREATISAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR Glycoprotein; Signal; Lectin.
SQ SEQUENCE 165 AA; 18672 MW; 9861EB236B82CF8A CRC64;
FT SIGNAL 1 21
FT CHAIN 22 165 LITHOSTATHINE.
FT DOMAIN 33 163 C-TYPE LECTIN (LONG FORM).
FT DISULFID 35 46 BY SIMILARITY.
FT DISULFID 63 161 BY SIMILARITY.
FT DISULFID 136 153 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 165 AA; 18672 MW; 9861EB236B82CF8A CRC64;

Query Match 13.4%; Score 137; DB 1; Length 165;
Best Local Similarity 27.2%; Pred. No. 3.8e-06;
Matches 43; Conservative 23; Mismatches 68; Indels 24; Gaps 7;

Qy 49 VLLSVLYQWLTCGSSNYSCASCPs-----CPDRMKYGNHCYFVSVEKDWNSSLEFCL 104
Db 8 ILLSLCLM---VLSPSQGEAEEDLPsARITCPESGNAYSSCYFYMEDHLsWAEADLFQC 64
Qy 105 ARDS-HLLVITDQEMSLQLQVFLSE-----AFQVIGL---PNSCWREDGSPINP---- 151
Db 65 NMNSGYLVSLVSQAEGNFLASLIKESGTTAAVWVIGLHDPKNNRRHWWSSGSLFLYKSWD 124
Qy 152 SRISSNSFVQPCGAINKNG-----LQASSCEVPLHGVCX 185
Db 125 TGYNNNSRGYCVSVTSNSGYKKWRDNSCDALQSLFVCK 162

RESULT 12
ANP_HEMAM STANDARD; PRT; 163 AA.
AC P05140;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Antifreeze protein precursor (AFP).
OS Hemitripterus americanus (Sea raven).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Hemitriptera; Hemitriptera; Hemitriptera; Hemitriptera;
ON NCBI_TaxID=8094;
RX SEQUENCE FROM N.A.
RX MEDLINE=87057207; PubMed=3782083;
RA Ng N.F.L., Trinh K.-Y., Hew C.-L.;
RT "Structure of an antifreeze polypeptide precursor from the sea raven,
RT Hemitripterus americanus.";
RL J. Biol. Chem. 261:15690-15695(1986).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90036986; PubMed=2572595;
RA Hayes P., Scott G.K., Ng N.F.L., Hew C.-L., Davies P.L.;
RT "Cystine-rich type II antifreeze protein precursor is initiated from
RT the third AUG codon of its mRNA.";
RL J. Biol. Chem. 264:18761-18767(1989).
RN [3]
RP DISULFIDE BONDS, AND SIMILARITY TO C-TYPE LECTINS.
RX MEDLINE=92355557; PubMed=1644794;
RA Ng N.F.L., Hew C.-L.;
RT "Structure of an antifreeze polypeptide from the sea raven. Disulfide
RT bonds and similarity to lectin-binding proteins.";
RL J. Biol. Chem. 267:16069-16075(1992).
RN [4]
RP STRUCTURE BY NMR, AND REVISIONS TO DISULFIDE BONDS.
RX MEDLINE=98206886; PubMed=9537986;
RA Gronwald W., Loewen M.C., Lix B., Daugulis A.J., Soennichsen F.D.,
RA Davies P.L., Sykes B.D.;
RT "The solution structure of type II antifreeze protein reveals a new
RT member of the lectin family.";
RL Biochemistry 37:4712-4721(1998).
CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC -!- SIMILARITY: BELONGS TO THE TYPE-II AFP FAMILY. TYPE 2 AFP ARE
CC CYSTEINE-RICH.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02593; AAA49617.1; ALT_INIT.
DR EMBL; J05100; AAA49618.1; -
DR PIR; A34313; A34313.
DR PDB; 2AFP; 23-DEC-98.
DR InterPro; IPR002353; Antifreeze2.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR Antifreeze protein; Lectin; Signal; 3D-structure.
FT SIGNAL 1 17
FT PROPEP 18 34
FT CHAIN 35 163 ANTIFREEZE PROTEIN.
FT DOMAIN 39 163 C-TYPE LECTIN (LONG FORM).
FT DISULFID 41 52
FT DISULFID 69 159
FT DISULFID 103 134
FT DISULFID 123 145
FT DISULFID 135 151
FT CONFLICT 38 38 P -> G (IN REF. 2).
FT STRAND 52 53
FT HELIX 62 72

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FT STRAND 75 76
FT HELIX 83 91
FT STRAND 96 96
FT STRAND 101 101
FT STRAND 110 110
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 138
FT STRAND 146 146
FT STRAND 149 149
FT STRAND 159 161
SQ SEQUENCE 163 AA; 17509 MW; 52C2D284F65E8A47 CRC64;

Query Match
Best Local Similarity 13.3%; Score 136; DB 1; Length 163;
Matches 26; Conservative 10; Mismatches 42; Indels 4; Gaps 2;

QY 73 PSCPDRWMKYGNHCYFVSVEEKDWNSSLEFLCLARDGHLVITDQMSLLQVFLSEAFQW 132
Db 39 PNCPCAGWQPLGDRCIYIETATWALAEATNCMLGGLASIHQSQEHSPFQT-LNAGVW 97

QY 133 IG---LRNNSGWRWEGDGPLNF 151
Db 98 IGGSAQLQAGAWTWSGDTMNF 119

RESULT 13
LITH_BOVIN STANDARD; PRT; 175 AA.
AC P23132;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lithostathine precursor (pancreatic stone protein) (PSP) (Pancreatic
DE lithostathine) (PTP) (Islet of Langerhans regenerating protein) (REG)
DE (Islet cells regeneration factor) (ICRF).
GN PTP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368981; PubMed=2394826;
RA de la Monte S.M., Ozturk M., Wands J.R.;
RT "Enhanced expression of an exocrine pancreatic protein in Alzheimer's
RL disease and the developing human brain.";
RL J. Clin. Invest. 86:1004-1013(1990).
RN [2]
RP SEQUENCE OF 38-138 AND 141-175.
RX MEDLINE=91197388; PubMed=2085387;
RA Cai L., Harris W.R., Marshak D.R., Gross J., Crabb J.W.;
RT "Structural analysis of bovine pancreatic thread protein.";
RL J. Protein Chem. 9:623-632(1990).
RN [3]
RP SEQUENCE OF 38-85 AND 141-175.
RX MEDLINE=85298214; PubMed=3862086;
RA Gross J., Brauer A.W., Bringham R.F., Corbett C., Margolies M.N.;
RT "An unusual bovine pancreatic protein exhibiting pH-dependent
RT globule-fibril transformation and unique amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631(1985).
CC -1- FUNCTION: Might act as an inhibitor of spontaneous calcium
CC carbonate precipitation.
CC -1- SUBUNIT: Cleaved to give an A chain and a B chain joined by a
CC disulfide bond.
CC -1- TISSUE SPECIFICITY: In pancreatic acinar cells.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR DR M59794; AAA30750.1; -.
DR PIR; A37194; A37194.
DR HSSP; P05451; LODD.
DR InterPro; IPR001304; Lectin.C.
DR InterPro; IPR003990; Pancreatins.ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Glycoprotein; Signal; Lectin.
FT SIGNAL 1 26
FT PROPEP 27 37
FT CHAIN 38 175
FT CHAIN 38 138
FT CHAIN 141 175
FT DOMAIN 38 173
FT DISULFID 40 51
FT DISULFID 68 171
FT DISULFID 146 163
FT CONFLICT 84 85
SQ SEQUENCE 175 AA; 19334 MW; C270EE70B7E91D6A CRC64;

Query Match
Best Local Similarity 13.1%; Score 134.5; DB 1; Length 175;
Matches 48; Conservative 27; Mismatches 63; Indels 37; Gaps 9;

QY 42 TGLG--LTAVLTLVLLVLYQWILCOGSSNYSCASCP-----SCPDRWMKYGNHCYFVSVEEKD 95
Db 4 SLGLPRLSWMLLSCLM---LLSQIQGNSQKQLPSARISCPGSMAYRSHCYALFKTPKT 60

QY 96 WNSLSEFLCLARDGHLVITDQMSLLQVFL-----SEAFQWIGLR-----NNSGW 141
Db 61 WMDADIACOKRPSGHLVSVLGAESFVASLVRNNTQSDIWLGHDTGSEANAGW 120

QY 142 RWEDGSPLNF-----SRISNSFVQTCGAINKNG-----LQASSCEVPLHGVC 185
Db 121 EWISNDVLNVAVWETDPAALISPGY---CGSLSRSSGYLKWRDHNCNLNLPYVCK 172

RESULT 14
PAP2_MOUSE STANDARD; PRT; 175 AA.
AC O09037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet
DE of Langerhans regenerating protein 3) (REG 3) (REG III-alpha).
GN PAP2 OR REG3A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas;
RX MEDLINE=97208868; PubMed=9055810;
RA Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL Gene 183:153-168(1997).
CC -1- FUNCTION: Might be a stress protein involved in the control of
CC bacterial proliferation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Small intestine and pancreas.
CC -1- DISEASE: Overexpressed during the acute phase of pancreatitis.

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CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D63356; BAA18925.1; -.
CC EMBL; D63357; BAA18926.1; -.
CC EMBL; D63358; BAA18927.1; -.
CC HSSP; P05451; 1LIT.
CC MCD; MGI:109408; Reg3a.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR003990; Pancreatins_ac.
CC Pfam; PF00059; lectin_c; 1.
CC PRINTS; PR01504; PNCREATITISAP.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC SIGNAL; 1 26
CC Signal; Lectin; Inflammatory response; Acute phase; Multigene family.
KW CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 2.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19539 MW; 3E311B3976E80F11 CRC64;

Query Match 13.1%; Score 134.5; DB 1; Length 175;
Best Local Similarity 28.2%; Pred. No. 7.1e-06;
Matches 49; Conservative 21; Mismatches 69; Indels 35; Gaps 8;

Qy 41 ITLGLLFAVLVLLVLYQWILQSGNYSYCASCSP--SCPDRMKNYGNHCYFSVEEKDWN 98
Db 5 LVLSISWMLLSCLLFVQV-QGEDFQKEVPSPTSCPMGYKAYRSHCYALVMTPKSWFQ 63
Qy 99 SLEFLCLARDS-HLIVTDNQEMSLLOVFLSFAF-----CWIGLR-----NNSGRWE 144
Db 64 ADLVQKRRPSGHLVLSLGGSEAFVSFLVNGRVNVDYQDIWIGLHPTNGQQPNGGGWEWS 123
Qy 145 DGSPLNF-----SRISNSSNFVOTCGAINKNGLOQASS-----CEVPLHGVCCK 185
Db 124 NSDVLYNLWNGDPSSTVNRGHCSS-----LTASSGFLKWDGYCDGLTLPVCK 172

RESULT 15
MMHB AGKHA STANDARD; PRT; 146 AA.
AC Q9YI92;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mamushigin beta chain precursor.
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Gloydius.
OC NCBI_TaxID=242054;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=98319530; PubMed=9657448;
RA Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
RA Suzuki M., Matsui T., Titani K., Yoshioka A.;
RT "The cDNA cloning and molecular characterization of a snake venom
RT platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
RT halys blomhoffii venom.";
RL Thromb. Haemost. 79:1199-1207(1998).
CC -!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet
CC aggregation at low-shear stress. At high-shear stress, aggregation
```

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CC is inhibited.
CC -!- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
CC linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=15413; MW_ERR=6; METHOD=Electrospray;
CC RANGE=24-146.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; AB019616; BAA34425.1; -.
CC HSSP; P23807; 1LXX.
CC GO; GO:0005576; C:extracellular; IC.
CC GO; GO:0007596; P:blood coagulation; IDA.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC Blood coagulation; Lectin; Signal.
FT SIGNAL 1 23
FT CHAIN 24 146 MAMUSHIGIN BETA CHAIN.
FT DOMAIN 32 143 C-TYPE LECTIN.
FT DISULFID 25 36 BY SIMILARITY.
FT DISULFID 53 142 BY SIMILARITY.
FT DISULFID 98 98 INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
FT DISULFID 119 134 (BY SIMILARITY).
FT DISULFID 146 AA; 17064 MW; 9EDA84BDC24E76D CRC64;
SQ SEQUENCE 146 AA; 17064 MW; 9EDA84BDC24E76D CRC64;

Query Match 13.1%; Score 134; DB 1; Length 146;
Best Local Similarity 28.6%; Pred. No. 6.5e-06;
Matches 36; Conservative 18; Mismatches 50; Indels 22; Gaps 6;

Qy 75 CPDRMKNYGNHCYFSVEEKDWNSSLFCL--ARDSHLVITDNGE---MSLLQVFLSE 128
Db 25 CPDWSSEYEGHCYRVFQKEMTWEDAEKFCQQRKESHLVSPHSSEEDFVVVSMTPILKY 84
Qy 129 AFQWIGLRNKGW-----RWEDGSPFNFSRISNSSNFVOTCGAI---NKNGLOQASSCEVP 179
Db 85 DFVWIGL--NNIWNECVWETDG-----TRLUSHNAWITESECIAAKTIDNWLSPCST 137
Qy 180 LHGYCK 185
Db 138 YNVVCK 143

Search completed: August 10, 2004, 16:34:04
Job time : 14 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:29:18 ; Search time 37 Seconds
(without alignments)
1611.701 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLELPTATQAN.....GLQASSCEVLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 398377

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1023	100.0	189	4	O43198	O43198 homo sapien
2	1007	98.4	189	4	O75613	O75613 homo sapien
3	548.5	53.6	188	11	O88713	O88713 mus musculus
4	525.5	51.4	188	11	Q64335	Q64335 rattus norv
5	225	22.0	181	4	Q9NZS1	Q9NZS1 homo sapien
6	194.5	19.0	178	11	Q912W9	Q912W9 mus musculus
7	189.5	18.5	179	6	Q8MJ13	Q8MJ13 pongo pygma
8	189.5	18.5	179	6	Q8MYH8	Q8MYH8 pongo pygma
9	187	18.3	179	11	O35778	O35778 rattus norv
10	186.5	18.2	179	6	Q8MYH9	Q8MYH9 pongo pygma
11	186.5	18.2	179	6	Q8MJ14	Q8MJ14 pongo pygma
12	185	18.1	132	11	Q834K5	Q834K5 rattus norv
13	185	18.1	133	6	Q9GK90	Q9GK90 macaca mula
14	184.5	18.0	159	6	Q8SPX0	Q8SPX0 sus scrofa
15	184	18.0	183	13	Q802S7	Q802S7 gallus gall
16	183.5	17.9	179	11	O54708	O54708 mus musculus

17	183.5	17.9	179	11	O54707	O54707 mus musculus
18	180.5	17.6	158	11	Q80235	Q80235 mus musculus
19	175.5	17.2	168	11	Q9JKF2	Q9JKF2 mus musculus
20	175.5	17.2	183	6	Q95J54	Q95J54 pan troglod
21	174.5	17.1	161	6	Q95JG4	Q95JG4 bos taurus
22	173	16.9	175	11	Q9JKF3	Q9JKF3 mus musculus
23	167.5	16.4	185	6	Q9MZJ6	Q9MZJ6 macaca mula
24	163.5	16.0	80	6	Q95UG6	Q95UG6 bos taurus
25	163.5	16.0	80	6	Q95JG5	Q95JG5 bos taurus
26	162.5	15.9	164	11	Q9EP94	Q9EP94 mus musculus
27	162	15.8	156	11	Q7TSP6	Q7TSP6 mus musculus
28	161.5	15.8	162	6	Q8MJH4	Q8MJH4 pongo pygma
29	161.5	15.8	162	6	Q8MJH3	Q8MJH3 pongo pygma
30	161.5	15.8	173	4	Q9HD37	Q9HD37 homo sapien
31	160.5	15.7	162	6	Q8MHY4	Q8MHY4 pongo pygma
32	160	15.6	146	13	Q7T045	Q7T045 vipera lebe
33	159.5	15.6	165	6	Q9GLF4	Q9GLF4 sus scrofa
34	159	15.5	188	4	Q9NY25	Q9NY25 homo sapien
35	157	15.3	137	4	Q8I2E9	Q8I2E9 homo sapien
36	156	15.2	154	4	Q8WUF7	Q8WUF7 homo sapien
37	155.5	15.2	142	11	Q8V119	Q8V119 mus musculus
38	155.5	15.2	142	11	Q8BHK7	Q8BHK7 mus musculus
39	155.5	15.2	187	4	Q9UKQ0	Q9UKQ0 homo sapien
40	154	15.1	182	11	Q61972	Q61972 mus musculus
41	153.5	15.0	142	11	Q8C786	Q8C786 mus musculus
42	152.5	14.9	185	6	Q9GLF3	Q9GLF3 sus scrofa
43	150	14.7	168	4	Q96PA7	Q96PA7 homo sapien
44	147	14.4	134	5	Q9XYX3	Q9XYX3 hydra magni
45	147	14.4	176	11	Q9D8Q7	Q9D8Q7 mus musculus

ALIGNMENTS

RESULT 1

O43198 PRELIMINARY; PRT; 189 AA.
ID O43198
AC O43198
DT 01-JUN-1998 (TREMREL. 06, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Mast cell function-associated antigen.
GN MAFA
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98438735; PubMed=9765598;
RA Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAFA has alternatively spliced variants.";
RL Biochim. Biophys. Acta 1399:209-212(1998).
DR EMBL: AF034952; AAC34731.1;
DR GO: GO:0016021; C:integral to membrane; TAS.
DR GO: GO:0003793; F:defense/immunity protein activity; TAS.
DR GO: GO:0005530; F:lectin; TAS.
DR GO: GO:0004872; F:receptor activity; TAS.
DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR GO: GO:0006968; P:cellular defense response; TAS.
DR GO: GO:0006954; P:inflammatory response; TAS.
DR InterPro: IPR001304; Lectin_c; 1.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 189 AA; 21073 MW; 15E042AD40B2B4F6 CRC64;

Query Match 100.0%; Score 1023; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDSVIYSMLELPTATQANDYGPQKSSSRKPSCSCLVAITLGLTAVLLSVLLQWIL 60

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Db 1 MTDSVIYMLELPTATQNDYGPQOKSSSSKPCSCLCVATLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDPRMWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
Db 61 CQGSNYSTCASCPCPDPRMWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
QY 121 LLOQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
Db 121 LLOQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

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RESULT 2

```

O75613 PRELIMINARY; PRT; 189 AA.
AC O75613;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ITIM-containing receptor MAFA-L.
GN MAFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
RT complex and expressed by basophils and NK cells.";
RL Eur. J. Immunol. 28:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
DR EMBL; AF081675; AAC32200.1; -.
DR EMBL; AF097358; AAC03719.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 189 AA; 21205 MW; FA9023F1523656A8 CRC64;

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Query Match 98.4%; Score 1007; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 4.3e-103;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDSVIYMLELPTATQNDYGPQOKSSSSKPCSCLCVATLGLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYMLELPTATQNDYGPQOKSSSSKPCSCLCVATLGLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCPDPRMWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
Db 61 CQGSNYSTCASCPCPDPRMWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
QY 121 LLOQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
Db 121 LLOQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HWVCCKVRL 189

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RESULT 3

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O88713 PRELIMINARY; PRT; 188 AA.
AC O88713;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-
DE like receptor G1).
GN KLRG1 OR MAFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raullet D.H.;
RT "2F1 antigen, the mouse homolog of the rat 's1', is a lectin-like type
RT II transmembrane receptor expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP SEQUENCE OF 2-188 FROM N.A.
RA Blaser C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvevTACFeR; TISSUE=Spleen;
RX MEDLINE=21115136; PubMed=11220622;
RA Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
DR EMBL; AF097357; AAD03718.1; -.
DR EMBL; AJ010751; CAA09342.1; -.
DR EMBL; AF317727; AAK40082.1; -.
DR MGI; MGI:1355294; KLRG1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR LECTIN; Receptor.
SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match 53.6%; Score 548.5; DB 11; Length 188;
Best Local Similarity 55.6%; Pred. No. 2.1e-52;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDSVIYMLELPTATQNDYGPQOKSSSSKPCSCLCVATLGLTAVLLSVLLYQWIL 60
Db 1 MADSSITSLPEAPQVQDESRLKAVLRPHLSRFAMVALGLLTIVILSLMYQRIL 60
QY 61 CQGSNYSTCASCPCPDPRMWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
Db 61 CQGSNYSTCASCPCPDPRMWMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
QY 121 LLOQVFLSEAFQWIGLRNNSGWRWEDGSPINFSRISNSSNFVQTCGAINKNGLOASSCEVPL 180
Db 121 LQGEYLGQDFYWIQLRNLIDGWRWEGPALSL-RILTNSLIQRCAIHRNGLQASSCEVAL 179
QY 181 HGVCCKV 187
Db 180 QWICKV 186

RESULT 4
Q64335 PRELIMINARY; PRT; 188 AA.
ID Q64335
AC Q64335;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAFA protein.
GN MAFA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=Testis;
RA Bocek Jr P., Gutmann M.D., Pecht I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=96016176; PubMed=7568140;
RA Gutmann M.D., Tal M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
RL another C-type lectin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; -.
DR EMBL; X97192; CAA65829.1; JOINED.
DR EMBL; X97193; CAA65829.1; JOINED.
DR EMBL; X97194; CAA65829.1; JOINED.
DR EMBL; X97195; CAA65829.1; JOINED.
DR EMBL; X97812; CAA56208.1; -.
DR PIR; I59421; I59421.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;

Query Match 51.4%; Score 525.5; DB 11; Length 188;
Best Local Similarity 53.5%; Pred. No. 7.2e-50;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVLYSMELPTAQNDYGPQKSSSKPSCSLVAITLGLTAVLLSVLLYQWIL 60
DB 1 MADNSYSTSLPAPRPVQDSSRWKAVLHRPCVSVLVMVALGLLTILMSLLYQRTL 60
QY 61 CGSNYSTCASCPDRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120
DB 61 CGSGKGFMCQRCRPNLMWRNGSHCYFSMERKDNSSLKFCADKGSLLHTPPDQGVN 120
QY 121 LLQVFLSEAFPCWITGLRNNSGWRWEDGSPNFSFVQTCGAINKNGLOASSCEVPL 180
DB 121 LFQEVYGEDFYWILGLRIDGWRWEDGFALSLS-ILNSVVKCGTHRCGLHASSCEVAL 179
QY 181 HGVCVKV 187
DB 180 QWICEKV 186

RESULT 5
Q9NZS1 PRELIMINARY; PRT; 181 AA.
AC Q9NZS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin-like receptor Fl, splice variant 1 KLRP1-s1.
GN KLRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20135860; PubMed=10671213;
RA Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,

Fernandez-Ruiz E.;
"Human KLRP1, a novel member of the killer cell lectin-like receptor
gene family: molecular characterization, genomic structure, physical
mapping to the NK gene complex and expression analysis.";
Eur. J. Immunol. 30:568-576(2000).
DR EMBL; AF175207; AAF37805.1; -.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 21204 MW; 64642240CAE1B551 CRC64;

Query Match 22.0%; Score 225; DB 4; Length 181;
Best Local Similarity 33.6%; Pred. No. 1.1e-16;
Matches 51; Conservative 26; Mismatches 45; Indels 30; Gaps 6;

QY 44 GLTAVLLSVLLYQWILCOGSNYSTCASCPDRMKYGNHCYFVSVEEKDWNSSLEFC 103
DB 49 GLTTLTSLILL--VLQC-----SEWLKYQKCYFNSNEMKWSDSYVYC 92
QY 104 LARDSHLLVITDQEMSLLQVFLSBA-FCWIGLRNNS---GWRWEDGSPNFSRISNSF 159
DB 93 LERKSHLLIIHDQLEMAFIQKNLRQLNYVYVIGLFTSLKMTWTVDGSPID----SKIFF 148
QY 160 VQ-----TCGAINKNGLOASSCEVPLHGVCX 185
DB 149 IKGPAKENSAAIKESKIFSETCSSVFKWICQ 180

RESULT 6
Q91ZW9 PRELIMINARY; PRT; 178 AA.
AC Q91ZW9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR2.
GN CD209C OR SIGNR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX PubMed=11581173;
RA Park C.G., Takahara K., Umemoto E., Yashima Y., Matsubara K.,
RA Matsuda Y., Clausen B.E., Inaba K., Steinman R.M.;
RT "Five mouse homologues of the human dendritic cell C-type lectin, DC-
RT SIGN. ";
RL Int. Immunol. 13:1283-1290(2001).
DR EMBL; AF373410; AAL13236.1; -.
DR MGD; MGI:2157945; Cd209c.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 178 AA; 21245 MW; 034P94CE02BD9032 CRC64;

Query Match 19.0%; Score 194.5; DB 11; Length 178;
Best Local Similarity 31.0%; Pred. No. 2.6e-13;
Matches 39; Conservative 23; Mismatches 53; Indels 11; Gaps 3;

QY 72 CPSCPDPMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLQVFLSE-AF 130
DB 45 CRPCPDWTVFQGCYFFSKFQGNWDSYNACRKLDAQLVVKSDDEQSFLOQTSKEGY 104
```


Matches 37; Conservative 20; Mismatches 52; Indels 8; Gaps 3;
 QY 74 SCPDRWMYGNHCYFVSVEEKDWNSSLEFCLARDSHLIVITDNOE-MSLLQVFLSEAFQW 133
 Db 17 SKNEWFSYNGKCVFFSTTTKTWALAQSCSDRTAVIDSEKDMAFLEKRYAGLKHVI 76
 QY 134 GLRNSG--WRWEDGSPLN--FSRISNSFVQTCGAINKNGLOASCEVPLHGVCCK 186
 Db 77 GLRNEASQTKWANGKEFNWFTGVS---KKCVSLNHTDVASVDCENLHWICK 129
 RESULT 13
 Q9GK90
 ID Q9GK90 PRELIMINARY; PRT; 163 AA.
 AC Q9GK90;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NK2-C.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21158386; PubMed=11261935;
 RA Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
 RT "Selective expression of NK2-A and NK2-C mRNAs and novel alternative
 RT splicing of 5' exons in rhesus monkey decidua."
 RL Immunogenetics 53:69-73(2001).
 DR EMBL; AF294887; AAC34499.1; -.
 DR HSSP; P22897; 1REG.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 163 AA; 18651 MW; DA2C8EA027A4D543 CRC64;

Query Match 18.1%; Score 185; DB 6; Length 163;
 Best Local Similarity 31.4%; Pred. No. 2.7e-12;
 Matches 43; Conservative 24; Mismatches 60; Indels 10; Gaps 4;
 QY 57 QWILCOGNSYSTCAS-----CPSCDRWMYGNHCYFVSVEEKDWNSSLEFCLARDSHL 111
 Db 26 QKVLQNNSPNTETQVRHCHGCPPEWITYNSCYIGKEKRTWASLLACTSKNSILL 85
 QY 112 VITDNOE-MSLLQVFLSEAFQWIGL--RNSGWRWEDGSPLNFSRISNS--FVQTCGAINK 168
 Db 86 SIDNEEMKFLTALPSS--WIGVFRNSHHPPWVTNGLTFKHEIKNSDNEHNCAMLHA 143
 QY 169 NGLQASCEVPLHGVCCK 185
 Db 144 RGLKSNQCESTVIYHCK 160

RESULT 14
 Q8SPX0
 ID Q8SPX0 PRELIMINARY; PRT; 159 AA.
 AC Q8SPX0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Type II membrane protein CD69 splice variant.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 SEQUENCE FROM N.A.
 RA Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
 Rothschild M.F., Kim Y.B.;

"Molecular cloning, expression pattern, and chromosomal mapping of pig
 CD69."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF484234; AAL91547.1; -.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 159 AA; 18056 MW; A19C3EEBAE92AA69 CRC64;
 Query Match 18.0%; Score 184.5; DB 6; Length 159;
 Best Local Similarity 32.2%; Pred. No. 2.9e-12;
 Matches 38; Conservative 19; Mismatches 52; Indels 9; Gaps 4;
 QY 74 SCPDRWMYGNHCYFVSVEEKDWNSSLEFCLARDSHLIVITDNOE-MSLLQVFLSEAFQW 132
 Db 43 SCPDDWIGYQTKCYFISKTKYNTLAQSCFCKHKGATLALLEKEDMVFLQKHVGRABHW 102
 QY 133 IGLRNSG--WRWEDGSPLN--FSRISNSFVQTCGAINKNGLOASCEVPLHGVCCK 186
 Db 103 IGLKNEVGQTKWNSGKFEFNWFKLTGS----KNCPLNSTEVSMECKNLHWICK 156

RESULT 15
 Q802S7
 ID Q802S7 PRELIMINARY; PRT; 183 AA.
 AC Q802S7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE C-type lectin.
 GN Y-LECL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 SEQUENCE FROM N.A.
 RA Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
 RA Kaiser P.;
 RT "Analysis of part of the chicken Rfp-Y region reveals two novel lectin
 RT genes, the first complete genomic sequence of a class I alpha-chain
 RT gene, a truncated class II beta-chain gene, and a large CRI repeat."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ277927; CAD61337.1; -.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 SQ SEQUENCE 183 AA; 20011 MW; 725DB7845867D341 CRC64;

Query Match 18.0%; Score 184; DB 13; Length 183;
 Best Local Similarity 29.3%; Pred. No. 3.9e-12;
 Matches 51; Conservative 20; Mismatches 57; Indels 46; Gaps 6;
 QY 22 YGPQQKSSSKPSCSGLVATLGLTAVLLSVLLYQWILCOGNSYSTCASCPDRWVK 81
 Db 33 HGTGRRRSRVOLIAACALGTLSLVLVISTDFAH-----ACPNAWVG 75
 QY 82 YGNHCYFVSVEEKDWNSSLEFCLARDSHLIVITDNOE-MSLLQVFLSEAFQWIGL---RNN 138
 Db 76 FQGKCYLLSKEENDWNSSREHCNAGASLATIGSAEEMDFMMRFQGPANCMWIGHWEED 135
 QY 139 SGWRWED-----GSPLNFSRISNSFVQTCG-----INKNGLOASCEV 178
 Db 136 ALMTWSNVTFTNWRGSP-----SPSQCTGGAAPFSSLLGTGL---SCEV 177

Search completed: August 10, 2004, 16:34:58
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:19:43 ; Search time 53 Seconds
(without alignments)
1007.575 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 WTDSVIYSMLPLPTATQAN.....GLQASCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1084940

Minimum DB seq length: 0
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1023	100.0	189	2	Aaw88265 Human mas
2	1023	100.0	189	4	Aae11759 Human mas
3	1007	98.4	189	7	Add25635 Binding d
4	548.5	53.6	188	4	Aae11760 Mouse mas
5	525.5	51.4	188	2	Aar77033 Mammalian
6	525.5	51.4	188	2	Aaw88277 Rat mast
7	525.5	51.4	188	4	Aae11761 Rat mast
8	431	42.1	99	2	Aaw88267 Human MAF
9	370.5	36.2	114	2	Aar77472 Partial s
10	306.5	30.0	70	2	Aaw88266 Human MAF
11	217	21.2	35	4	Aam14192 Peptide #
12	217	21.2	35	4	Abb33139 Peptide #
13	217	21.2	35	4	Aam26602 Peptide #
14	217	21.2	35	4	Abp27967 Human pep
15	217	21.2	35	4	Abb18604 Protein #
16	217	21.2	35	4	Aam66323 Human bon
17	217	21.2	35	4	Aam53935 Human bra
18	217	21.2	35	4	Abg47989 Human liv
19	217	21.2	35	4	Aam01928 Peptide #
20	217	21.2	35	5	Abg35971 Human pep
21	216.5	21.2	182	4	Aau19660 Human nov
22	216.5	21.2	182	5	Abp47880 Human pol
23	216.5	21.2	182	7	Adc10842 Human ext
24	196.5	19.2	179	2	Aaw64791 Human Kp4
25	196.5	19.2	179	2	Aaw40222 CD94. 7/1

ALIGNMENTS

```

RESULT 1
AAW88265
ID AAW88265 standard; protein; 189 AA.
XX
AC AAW88265;
XX
DT 29-MAR-1999 (first entry)
XX
DE Human mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; splice variant; human;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 7..10
FT Modified-site /note= "ITIM motif"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site /note= "Asn is N-glycosylated"
WC9854209-A2.
03-DEC-1998.
29-MAY-1998; 98WO-GB001572.
31-MAY-1997; 97GB-00011148.
(PEPT-) PEPTIDE THERAPEUTICS LTD.
Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
WPI; 1999-059806/05.
N-PSDB; AAW84198.
New polypeptide having a sequence corresponding to human mast cell
function-associated antigen - useful in forming and manufacturing
pharmaceutical compositions in the treatment of inflammatory and allergic
diseases, and tumour growth.
Disclosure; Fig 1; 44pp; English.

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XX This is the amino acid sequence of human mast cell function- associated
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AA84198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC K0812 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AA88277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITAM) and
 CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see
 CC AA88266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AA88258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 XX

Sequence 189 AA;
 Query Match 100.0%; Score 1023; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITLGLLTAVLLSVLLYQWIL 60
 DB 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITLGLLTAVLLSVLLYQWIL 60
 QY 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 DB 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 QY 121 LLQVFLSEAFPCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 DB 121 LLQVFLSEAFPCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 2
 AAEL1759
 ID AAEL1759 standard; protein; 189 AA.
 XX
 AC AAEL1759;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human mast cell function associated antigen (MAFA) protein.
 XX
 KW Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 FA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX
 DR WPI; 2001-611482/70.
 DR N-PSDB; AAD18734.
 XX
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 PS Claim 10; Page 18; 49pp; English.
 XX

CC The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 XX

Sequence 189 AA;
 Query Match 100.0%; Score 1023; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.8e-98;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITLGLLTAVLLSVLLYQWIL 60
 DB 1 MTDVSIYMLELPTATQAQNDYGPQKSSSKSPSCSLVAITLGLLTAVLLSVLLYQWIL 60
 QY 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 DB 61 CQGSNYSTCASCPCDRWVKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
 QY 121 LLQVFLSEAFPCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 DB 121 LLQVFLSEAFPCWIGLRNNSGWRWEDGSPFNFSRISSNSFVOTCGAINKNGLOASSCEVPL 180
 QY 181 HGVCCKVRL 189
 DB 181 HGVCCKVRL 189

RESULT 3
 ADD25635
 ID ADD25635 standard; protein; 189 AA.
 XX
 AC ADD25635;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #95.
 XX
 KW Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 XX
 PN US2003118592-A1.
 XX
 PD 26-JUN-2003.
 XX
 PR 25-JUL-2002; 2002US-00207655.
 XX
 PR 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-00053530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 PA (GENE-) GENE-CRAFT INC.
 XX
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a

PT subject having or suspected of having a malignant condition or a B-cell

PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 196; 157pp; English.

XX The invention relates to a binding domain-immunoglobulin fusion protein

CC comprising a binding domain polypeptide that is fused to an

CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain

CC CH2 constant region polypeptide that is fused to the hinge region

CC polypeptide, and an immunoglobulin heavy chain CH3 constant region

CC polypeptide that is fused to the CH2 constant region polypeptide. The

CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin

CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge

CC region polypeptide, derived from (a) having 3 or more cysteine residues;

CC where the mutated human IgG1 immunoglobulin hinge region polypeptide

CC contains 2 cysteine residues, where the first cysteine is not mutated; a

CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from

CC (a) having 3 or more cysteine residues, where the mutated human IgG1

CC immunoglobulin hinge region polypeptide contains no more than one

CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region

CC polypeptide, derived from (a) having 3 or more cysteine residues; where

CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains

CC no cysteine residues. The binding domain-immunoglobulin fusion protein is

CC capable of at least one immunological activity comprising antibody

CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The

CC binding domain polypeptide is capable of specifically binding to an

CC antigen. Also included are an isolated polynucleotide encoding the

CC binding domain-immunoglobulin fusion protein, a recombinant expression

CC construct comprising the polynucleotide (operably linked to a promoter),

CC a host cell transformed or transfected with a recombinant expression

CC construct, producing the binding domain-immunoglobulin fusion protein, a

CC pharmaceutical composition comprising the binding domain-immunoglobulin

CC fusion protein or polynucleotide and a carrier, and treating a subject

CC having or suspected of having a malignant condition or a B-cell disorder.

CC The binding domain-immunoglobulin fusion protein is useful for treating a

CC subject having or suspected of having a malignant condition or a B-cell

CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,

CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple

CC sclerosis or autoimmune disease. The present sequence is a binding domain

CC -immunoglobulin fusion protein-associated protein sequence. Note: The

CC sequence data for this patent formed part of the printed specification

CC and is also available in electronic format directly from USPTO at

CC segdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not

CC identified the sequences in the printed specification by their SEQ ID

CC number therefore none of the sequences can be explicitly identified.

XX

SQ Sequence 189 AA;

Query Match 98.4%; Score 1007; DB 7; Length 189;

Best Local Similarity 98.4%; Pred. No. 8.5e-97;

Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVSYLMLEPTATQANDYGPQOKSSSPSCSLVAITLGLTAVLLSVLLYQWIL 60

DB 1 MTDVSYLMLEPTATQANDYGPQOKSSSPSCSLVAITLGLTAVLLSVLLYQWIL 60

QY 61 CQGSNYSTCASCPCSDRWKMYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

DB 61 CQGSNYSTCASCPCSDRWKMYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

QY 121 LQGVFLSEAFWIGLRNNSGWRWEDGSLNFRISNSFVQTCGAINKNGLQASSCEVPL 180

DB 121 LQGVFLSEAFWIGLRNNSGWRWEDGSLNFRISNSFVQTCGAINKNGLQASSCEVPL 180

QY 181 HGVCCKVRL 189

DB 181 HWVCCKVRL 189

RESULT 4

AAE11760

ID AAE11760 standard; protein; 188 AA.

XX

AC AAE11760;

XX

DT 18-DEC-2001 (first entry)

XX

DE Mouse mast cell function associated antigen (MAFA) protein.

XX

KW Mouse; pharmaceutical composition; mast cell function associated antigen;

KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;

KW immunosuppressive; cytostatic.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Domain 64..188

FT /note= "Extracellular domain"

XX

PN WO200170805-A2.

XX

PD 27-SEP-2001.

XX

PF 16-MAR-2001; 2001WO-US008596.

XX

PR 17-MAR-2000; 2000US-0190716P.

XX

PA (GEMI-) GEMINI SCI INC.

XX

PI Takahashi N, Mikayama T;

XX

DR WPI; 2001-611482/70.

DR N-PSDB; AAD18735.

XX

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic

PT activity of natural killer cell or T-cell, comprises an agent that binds

PT to mast cell function-associated antigen ligand on target cell.

XX

PS Example 1; Page 19; 49pp; English.

XX

CC The present invention relates to a pharmaceutical composition comprising

CC an agent which specifically binds to a mast cell function associated

CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural

CC killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA

CC ligand and a pharmaceutically acceptable excipient. The invention is

CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA

CC binding to a ligand on a target cell, by contacting the pharmaceutical

CC composition in vitro, ex vivo or in vivo by administering the composition

CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in

CC an amount sufficient to inhibit cell surface MAFA binding to the ligand

CC on the target cell. The agent or the composition is useful for treating a

CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic

CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible

CC tumour cell. The invention is also useful for inhibiting an activity of

CC NK cell or a T-cell. The present sequence is mouse MAFA protein

XX

SQ Sequence 188 AA;

Query Match 53.6%; Score 548.5; DB 4; Length 188;

Best Local Similarity 55.6%; Pred. No. 6.7e-49;

Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDVSYLMLEPTATQANDYGPQOKSSSPSCSLVAITLGLTAVLLSVLLYQWIL 60

DB 1 MADSSIIYTLPEAPQVQDESRLKXAVLHRLPHLSRFAMVALGLTAVLLSVLLYQWIL 60

QY 61 CQGSNYSTCASCPCSDRWKMYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMS 120

DB 61 CQGSNDSTCSHPCSPILWTRNGSHCYFVSMEKKDWNSSLKFCADKGSLLTTFPDNQGVK 120

QY 121 LQGVFLSEAFWIGLRNNSGWRWEDGSLNFRISNSFVQTCGAINKNGLQASSCEVPL 180

Db 121 LFGYLGQDFYWGILGRNIDGWRWGGPALSU-RILTNSLIQRCGAIHRNGLOASSCEVAL 179
QY 181 HGUCKV 187
:||||
Db 180 QWICKV 186

RESULT 5

AAR77033
ID AAR77033 standard; protein; 188 AA.

XX AC AAR77033;

XX DT 01-FEB-1996 (first entry)

XX DE Mammalian mast cell function-associated antigen (MAFA).

XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.

XX OS Rattus rattus.

XX PN WO9527734-A1.

XX PD 19-OCT-1995.

XX PF 06-APR-1995; 95WO-US004258.

XX PR 08-APR-1994; 94IL-00109257.

XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PA (RYCU/) RYCUS A.

XX PI Pecht I, Guthmann MD, Tal M;

XX DR WPI; 1995-366356/47.

XX DR N-PSDB; AAT01471.

XX PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.

XX PS Claim 12; Page 37; 54pp; English.

XX CC A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions

XX SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVIVSMLELPTAQAQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60

Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVMVALGLLTIVLMSLLYQRTL 60

QY 61 CQGSNYSTCASCPCSPDRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDNOEMS 120

Db 61 CCGSKGFWCQSCRCPNLWNRNGSHCYFVSFEKRDWNSSLKFCADKGSLLTFFPDNOGVN 120

QY 121 LLQVFLSEAFCTWIGLRNNSGRWEDGSLNFSRISSNFVQTCGAINKNGLOASSCEVPL 180

Db 121 LFQYVGEDFWIGLRIDGWRWEDGPALSUS-ILSNVSVQKCGTIHRCGLHASSCEVAL 179

QY 181 HGUCKV 187

Db 180 QWICEK 186

RESULT 6

AAW88277
ID AAW88277 standard; protein; 188 AA.

XX AC AAW88277;

XX DT 29-MAR-1999 (first entry)

XX DE Rat mast cell function-associated antigen (MAFA).

XX KW Mast cell function-associated antigen; MAFA; splice variant; rat;
KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

FT Modified-site 82..84

FT /note= "Asn is N-glycosylated"

FT Modified-site 97..99

FT /note= "Asn is N-glycosylated"

XX PN WO9854209-A2.

XX XX 03-DEC-1998.

XX XX 29-MAY-1998; 98WO-GB001572.

XX XX 31-MAY-1997; 97GB-00011148.

XX XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

XX DR WPI; 1999-059806/05.

XX DR N-PSDB; AAW84222.

XX PT New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.

XX PS Disclosure; Fig 4; 44pp; English.

XX CC This is the amino acid sequence of rat mast cell function-associated
CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and
CC basophils. The invention relates to cloning of the human MAFA molecule
CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)
CC of human MAFA that are not found in rat. Polypeptides and synthetic
CC peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
CC and polynucleotides encoding them, can be used in methods for the
CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
CC arthritis and asthma), and tumour growth

XX SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVIVSMLELPTAQAQNDYGPQKSSSKPSCSLVAITGLTAVLLSVLLYQWIL 60

Db 1 MADNSIYSTLELPAAPRVQDDSRWKVAVLHPCVSYLVVMVALGLLTIVLMSLLYQRTL 60

QY 61 CQGSNYSTCASCPCSPDRMKYGNHCYFVSVEEKDWNSSLFCLARDSHLLVITDNOEMS 120

Db 61 CCGSKGFWCQSCRCPNLWNRNGSHCYFVSFEKRDWNSSLKFCADKGSLLTFFPDNOGVN 120

QY 121 LLQVFLSEAFCTWIGLRNNSGRWEDGSLNFSRISSNFVQTCGAINKNGLOASSCEVPL 180

Db 121 LFQYVGEDFWIGLRIDGWRWEDGPALSUS-ILSNVSVQKCGTIHRCGLHASSCEVAL 179

QY 181 HGUCKV 187

:|||


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Db          91 HWVCKVRL 99
          | |||||
RESULT 9
AAR77472
ID AAR77472 standard; protein; 114 AA.
XX
XX
AC AAR77472;
XX
XX 01-FEB-1996 (first entry)
XX
XX
DE Partial sequence of mast cell function-associated antigen (MAFA).
XX
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergy; allergic;
KW prevention.
XX
XX Rattus rattus.
XX
XX WO9527734-A1.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1995; 95WO-US004258.
XX
XX 08-APR-1994; 94IL-00109257.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX (RYCU/) RYCU A.
XX
XX Pecht I, Guthmann MD, Tal M;
XX
XX WPI; 1995-366356/47.
XX
XX N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
XX Disclosure; Page 38; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
CC produced by recombinant techniques for use in the ligand- screening
CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions
XX
XX Sequence 114 AA;
Query Match 36.2%; Score 370.5; DB 2; Length 114;
Best Local Similarity 58.4%; Pred. No. 1.4e-30;
Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;
QY 75 CPDRWKYGNHCYFYFVEKDWNSLFCUARDSHLLVITDNQMSLLQVFLSEAFQWIG 134
Db 1 CPNLWNRNGSHCYFYFSEKEDWNSLKFCAKDGSHLLTFPDNQGWNLFQEVYGVDFYWG 60
QY 135 LRNNSGWRWEDGSPINFSTRSSNSFVQTCGINKNGLOASSCEYPLHGVCVKV 187
Db 61 LRIDGWRWEDGPALSLS-ILSNSVQKCGTHRCGLHASSCEVALQWICEKV 112
RESULT 10
AAW88266
ID AAW88266 standard; protein; 70 AA.
XX
XX
AC AAW88266;
XX
XX 29-MAR-1999 (first entry)
XX
XX Human MAFA splice variant huMAFA(E3-).
XX
XX Mast cell function-associated antigen; MAFA; huMAFA(E3-); splice variant;
KW
```

```
KW human; inflammation; allergy; asthma; rheumatoid arthritis; tumour;
KW therapy.
XX
XX Homo sapiens.
XX
XX WO9854209-A2.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-GH001572.
XX
XX 31-MAY-1997; 97GB-00011148.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX WPI; 1999-059806/05.
XX
XX N-PSDB; AAV84199.
XX
XX New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.
XX
XX Disclosure; Fig 2; 44pp; English.
XX
XX This is the amino acid sequence of human mast cell function- associated
CC antigen (MAFA) splice variant huMAFA(E3-). huMAFA(E3-) is a major
CC transcript, not found in rat, but highly expressed in human lung and
CC granulocyte-enriched blood cells. The truncated protein includes the
CC intracellular and transmembrane regions of human MAFA (see AAW88265),
CC followed immediately by a polyproline motif (see AAW88264) due to a
CC reading frameshift. This unique motif has been used to design peptides
CC (see AAW88259-64, AAW88268-72) that inhibit T cell antigen receptor-
CC dependent activation induced by interleukin-2 (IL2) secretion from human
CC Jurkat T cells or IgE dependent degranulation of rat basophil leukaemic
CC cells. Inhibition of IL2 production prevents T cell proliferation and
CC suppresses the immune system. These peptides, truncated MAFA polypeptides
CC including huMAFA(E3-), and polynucleotides encoding them, can be used be
CC used in compositions for the treatment of inflammatory and allergic
CC diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
XX
XX Sequence 70 AA;
Query Match 30.0%; Score 306.5; DB 2; Length 70;
Best Local Similarity 82.9%; Pred. No. 3.5e-24;
Matches 63; Conservative 1; Mismatches 5; Indels 7; Gaps 1;
QY 1 MTDSVIYSMLELPTATQANDYGPQOKSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60
Db 1 MTDSVIYSMLELPTATQANDYGPQOKSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL 60
QY 61 CQGSNYSTCASCPCSP 76
Db 61 CQ-----EPAPSPFP 69
RESULT 11
AAW14192
ID AAW14192 standard; protein; 35 AA.
XX
XX
AC AAW14192;
XX
XX 12-OCT-2001 (first entry)
XX
XX Peptide #626 encoded by probe for measuring cervical gene expression.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
XX Homo sapiens.
XX
```

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PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 19018; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAL10068-XAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 35 AA;
XX
XX Query Match 21.2%; Score 217; DB 4; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-15;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 64 SNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWS 98
XX ||||||||||||||||||||||||||||||||||
XX 1 SNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWS 35
XX
XX RESULT 12
XX ABB33139
XX ID ABB33139 standard; peptide; 35 AA.
XX
XX AC ABB33139;
XX
XX XX 04-FEB-2002 (first entry)
XX DT
XX DE Peptide #645 encoded by human foetal liver single exon probe.
XX
XX XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX OS Homo sapiens.
XX
XX PN WO200157277-A2.
XX
XX PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 26871; 654pp; English.
XX
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PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX Claim 27; SEQ ID NO 25774; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 35 AA;
XX
XX Query Match 21.2%; Score 217; DB 4; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-15;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 64 SNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWS 98
XX ||||||||||||||||||||||||||||||||||
XX 1 SNYSTCASCPCPDWRMKYGNHCYFVSVEEKDWS 35
XX
XX RESULT 13
XX AAM26602
XX ID AAM26602 standard; protein; 35 AA.
XX
XX AC AAM26602;
XX
XX DT 17-OCT-2001 (first entry)
XX
XX DE Peptide #639 encoded by probe for measuring placental gene expression.
XX
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200157272-A2.
XX
XX PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 26871; 654pp; English.
XX
```

CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 35 AA;

Query Match 21.2%; Score 217; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 SNYSTCASCPCPDPRWKMKGNYHCYFVSVEEKDWS 98
|||||
Db 1 SNYSTCASCPCPDPRWKMKGNYHCYFVSVEEKDWS 35

RESULT 14
ABB27967
ID ABB27967 standard; peptide; 35 AA.

XX
AC ABB27967;

DT 01-FEB-2002 (first entry)

DE Human peptide #618 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.

OS Homo sapiens.

PN WO200157271-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000662.

XX
PR 04-FEB-2000; 2000US-0180312P.

XX
PR 26-MAY-2000; 2000US-0207456P.

XX
PR 30-JUN-2000; 2000US-00608408.

XX
PR 03-AUG-2000; 2000US-00632366.

XX
PR 21-SEP-2000; 2000US-0234687P.

XX
PR 27-SEP-2000; 2000US-0236359P.

XX
PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful
XX for measuring gene expression in sample derived from human breast,
XX comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 10935; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a peptide

CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 35 AA;

Query Match 21.2%; Score 217; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 SNYSTCASCPCPDPRWKMKGNYHCYFVSVEEKDWS 98
|||||
Db 1 SNYSTCASCPCPDPRWKMKGNYHCYFVSVEEKDWS 35

RESULT 15
ABB18604
ID ABB18604 standard; protein; 35 AA.

XX
AC ABB18604;

DT 23-JAN-2002 (first entry)

DE Protein #603 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000666.

XX
PR 04-FEB-2000; 2000US-0180312P.

XX
PR 26-MAY-2000; 2000US-0207456P.

XX
PR 30-JUN-2000; 2000US-00608408.

XX
PR 03-AUG-2000; 2000US-00632366.

XX
PR 21-SEP-2000; 2000US-0234687P.

XX
PR 27-SEP-2000; 2000US-0236359P.

XX
PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.

XX Claim 15; SEQ ID NO 20374; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 35 AA;

Query Match

21.2%; Score 217; DB 4; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.1e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 SNYSTCASCPCPDRWMKYGNHCYFVSVEEKDWS 98
|||||
Db 1 SNYSTCASCPCPDRWMKYGNHCYFVSVEEKDWS 35
|||||

Search completed: August 10, 2004, 16:33:40
Job time : 54 secs

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Page 1 of 1 (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:05 ; Search time 53 Seconds
(without alignments)
1118.605 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYLMLELPTAQON.....GLQASSCEVPLGVCKKVRLL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 727970

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	9	US-09-811-367B-1
2	1007	98.4	189	14	US-10-207-655-196
3	548.5	53.6	188	9	US-09-811-367B-3
4	525.5	51.4	188	9	US-09-811-367B-5
5	217	21.2	35	9	US-09-864-761-33902
6	216.5	21.2	182	9	US-09-764-870-310
7	216.5	21.2	182	14	US-10-125-540-310
8	196.5	19.2	179	10	US-09-919-039-130
9	196.5	19.2	179	15	US-10-335-009-10
10	175	17.1	149	10	US-09-284-320-11
11	175	17.1	149	13	US-10-114-893-22
12	175	17.1	149	14	US-10-088-859-2
13	175	17.1	149	14	US-10-179-528-1
14	168.5	16.5	95	12	US-10-424-599-222182
15	168	16.4	149	9	US-09-944-807-6

16	168	16.4	149	15	US-10-335-009-6	Sequence 6, Appli
17	166	16.2	133	12	US-10-239-656-3	Sequence 3, Appli
18	166	16.2	143	12	US-10-239-656-2	Sequence 2, Appli
19	166	16.2	162	12	US-10-239-656-90	Sequence 90, Appl
20	165	16.1	140	9	US-09-764-870-340	Sequence 340, App
21	165	16.1	140	9	US-09-764-870-486	Sequence 486, App
22	165	16.1	140	14	US-10-125-540-340	Sequence 340, App
23	165	16.1	140	14	US-10-125-540-486	Sequence 486, App
24	165	16.1	189	9	US-09-764-870-487	Sequence 487, App
25	165	16.1	189	14	US-10-125-540-487	Sequence 487, App
26	163.5	16.0	94	9	US-09-764-870-466	Sequence 466, App
27	163.5	16.0	94	14	US-10-125-540-466	Sequence 466, App
28	162.5	15.9	165	10	US-09-759-130B-98	Sequence 98, Appl
29	162.5	15.9	165	16	US-10-741-790-98	Sequence 98, Appl
30	161	15.7	162	14	US-10-270-470-2	Sequence 2, Appli
31	161	15.7	181	13	US-10-114-893-22	Sequence 22, Appl
32	159.5	15.6	165	12	US-10-262-839-76	Sequence 76, Appl
33	159	15.5	187	14	US-10-212-198-9	Sequence 9, Appli
34	159	15.5	187	14	US-10-212-198-10	Sequence 10, Appl
35	159	15.5	188	10	US-09-759-130B-83	Sequence 83, Appl
36	159	15.5	188	16	US-10-741-790-83	Sequence 83, Appl
37	158.5	15.5	124	12	US-09-964-956-67	Sequence 67, Appl
38	158.5	15.5	124	12	US-10-072-012-836	Sequence 836, App
39	158.5	15.5	137	14	US-10-106-698-5855	Sequence 4, Appli
40	157.5	15.4	132	15	US-10-335-009-4	Sequence 108, App
41	157.5	15.4	145	10	US-09-759-130B-108	Sequence 108, App
42	157.5	15.4	145	16	US-10-741-790-108	Sequence 108, App
43	157	15.3	146	12	US-10-296-115-1275	Sequence 1275, Ap
44	155.5	15.2	143	9	US-09-764-870-471	Sequence 471, App
45	155.5	15.2	143	14	US-10-125-540-471	Sequence 471, App

ALIGNMENTS

RESULT 1

US-09-811-367B-1

; Sequence 1, Application US/09811367B

; Patent No. US20020155110A1

; GENERAL INFORMATION:

; APPLICANT: GEMINI SCIENCE, INC.

; APPLICANT: Takahashi, No, US20020155110A1uaki

; APPLICANT: Mikayama, Toshifumi

; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE

; FILE REFERENCE: 021286/0278719

; CURRENT APPLICATION NUMBER: US/09/811,367B

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 60/190,716

; PRIOR FILING DATE: 2000-03-17

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 189

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-811-367B-1

Query Match 100.0%; Score 1023; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.5e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDSVIYLMLELPTAQNDYGPQKSSSKSPSCSLVAITLGLTAVLLSVLLYQWIL	60
DB	1	MTDSVIYLMLELPTAQNDYGPQKSSSKSPSCSLVAITLGLTAVLLSVLLYQWIL	60
QY	61	CGGSNYSTCASCPDRWKYGNHCYFVSVEKDNSSLEFCCLARDSHLLVITDNQMS	120
DB	61	CGGSNYSTCASCPDRWKYGNHCYFVSVEKDNSSLEFCCLARDSHLLVITDNQMS	120
QY	121	LLQVFLSEAFWIGLRNNSGWEDGSPINFRISNSFVOTCGAINKKNGLQASSCEVPL	180
DB	121	LLQVFLSEAFWIGLRNNSGWEDGSPINFRISNSFVOTCGAINKKNGLQASSCEVPL	180

QY 181 HGVCCKVRL 189
| | | | |
Db 181 HGVCCKVRL 189
| | | | |
RESULT 2
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196

Query Match 98.4%; Score 1007; DB 14; Length 189;
Best Local Similarity 98.4%; Pred. No. 1.6e-95;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVSYMSLELPTATQANDYGPQOKSSSPSCSCLVAITGLTAVLLSVLLYQWIL 60
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Db 1 MTDVSYMSLELPTATQANDYGPQOKSSSPSCSCLVAITGLTAVLLSVLLYQWIL 60
| | | | |
QY 61 CGGSNYSTCASCPCDPRMKNYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
| | | | |
Db 61 CGGSNYSTCASCPCDPRMKNYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
| | | | |
QY 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
| | | | |
Db 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
| | | | |
QY 181 HGVCCKVRL 189
| | | | |
Db 181 HGVCCKVRL 189
| | | | |

RESULT 3
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3

Query Match 53.6%; Score 548.5; DB 9; Length 188;
Best Local Similarity 55.6%; Pred. No. 2.9e-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

RESULT 4
US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5

Query Match 51.4%; Score 525.5; DB 9; Length 188;
Best Local Similarity 53.5%; Pred. No. 6.7e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MTDVSYMSLELPTATQANDYGPQOKSSSPSCSCLVAITGLTAVLLSVLLYQWIL 60
| | | | |
Db 1 MADSIIYSTLELPAAPRVQDDSRWKVAVLHRCVSVLVMVALGLLTVILMSLLYQRTL 60
| | | | |
QY 61 CGGSNYSTCASCPCDPRMKNYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
| | | | |
Db 61 CGGSNYSTCASCPCDPRMKNYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
| | | | |
QY 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
| | | | |
Db 121 LLOVFLSEAFWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
| | | | |
QY 181 HGVCCKVRL 187
| | | | |
Db 180 QWICEKV 186
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RESULT 5
US-09-864-761-33902
; Sequence 33902, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1


```

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO. US20030108871A1 516300CDI
US-09-919-039-130

Query Match      19.2%; Score 196.5; DB 10; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAILGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGLILKNSFTKLSEPAFTPGPNIELQKSDCCSQCKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNEHRHLCAQSKSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEBHTAWLWENG 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDKRNRYICKQ 176

RESULT 9
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Boles, Kent S.
; APPLICANT: Portunello, Mathew A.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469887-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match      19.2%; Score 196.5; DB 15; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAILGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGLILKNSFTKLSEPAFTPGPNIELQKSDCCSQCKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNEHRHLCAQSKSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEBHTAWLWENG 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDKRNRYICKQ 176

; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-11

Query Match      17.1%; Score 175; DB 10; Length 149;
Best Local Similarity 32.2%; Pred. No. 6.8e-10;
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

QY 75 CPDRWMKYGNGHCYFVSVEEKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIG 134
DB 35 CPYDWIGFQNKCYFYFSEKGDWNSKYNCSQTHADLTITDNIENWFLRYYKCSDDHWIG 94
QY 135 L---RNNSGRWEDGSPNLSFNRSSISNSFVQTCGAINKNGLOASSCEVPLHGVCCK 186
DB 95 LKMAKNRTG-QWVDGA--TFYKFGMRGSECAVLSDDGAATARTCYTERKWKCR 146

RESULT 11
US-10-114-893-32
; Sequence 32, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Meirberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-32

Query Match      17.1%; Score 175; DB 13; Length 149;
Best Local Similarity 32.2%; Pred. No. 6.8e-10;
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

QY 75 CPDRWMKYGNGHCYFVSVEEKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIG 134
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; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 130
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO. US20030108871A1 516300CDI
US-09-919-039-130

Query Match      19.2%; Score 196.5; DB 10; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAILGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGLILKNSFTKLSEPAFTPGPNIELQKSDCCSQCKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNEHRHLCAQSKSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEBHTAWLWENG 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDKRNRYICKQ 176

RESULT 9
US-10-335-009-10
; Sequence 10, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Boles, Kent S.
; APPLICANT: Portunello, Mathew A.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469887-7
; CURRENT APPLICATION NUMBER: US/10/335,009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-009-10

Query Match      19.2%; Score 196.5; DB 15; Length 179;
Best Local Similarity 32.7%; Pred. No. 5.2e-12;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAILGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNGHCYFVSVE 92
DB 20 CLSLMA-TLGLILKNSFTKLSEPAFTPGPNIELQKSDCCSQCKWVGRCNCYFISSE 78
QY 93 EKDNSSLEFCLARDSHLLVITDNOEMSLLOVFLSEAFQWIGL---RNNSGRWEDGSP 149
DB 79 QKTWNEHRHLCAQSKSLLQLQNTDELDFMS--SSQQFYWIGLSYSEEBHTAWLWENG 136
QY 150 NFRSISNSF-----VOTCGAINKNG-LQASSCEVPLHGVCCK 186
DB 137 --SQYLFPSFETFNKNCIAYNPNGNALDESCEDKRNRYICKQ 176
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Db 35 CPYDWTFQNKCYFSEKEEDGNSSKYNCGSTQHADLTITDNEENWFLRRYKCCSDHWIG 94
 QY 135 L--RNNSGWRWEDGSPLEFSLSSNSFVOTCCAIKNKGLQASCEVPLHGVCVK 186
 Db 95 LKMAKNRTG-QWVDGA--TFTSKFGMRGEGAYLSDGGAATARCYTERKKWICK 146

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RESULT 12
US-10-088-859-2
; Sequence 2, Application US/10088859
; Publication No. US20030148468A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: NAGATA, Naoko
; APPLICANT: FUJIMURA, Naoko
; APPLICANT: KOBAYASHI, Midori
; APPLICANT: ITO, Koichi
; APPLICANT: ISHIZUKA, Yoshiko
; TITLE OF INVENTION: A Method for Producing an Antibody by Gene Immunization
; FILE REFERENCE: 2002-0400A/LC/00653
; CURRENT APPLICATION NUMBER: US/10/088,859
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: PCT/JP01/06371
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: JP2000-222743
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: JP2000-254407
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-088-859-2

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Query Match	17.1%	Score 175;	DB 14;	Length 149;
Best Local Similarity	32.3%;	Pred. No. 6.8e-10;		
Matches	37;	Conservative	24;	Mismatches 48; Indels 6; Gaps 3;
QY	75	CPDWRKYGHCYYFSSVEEDKNWSSLEFFCLARDSHLVIITDNQMSLLQVFLSEAFWC	134	
Dd	35	CPYDWIGFQNKCYFYFSKEEGDWSSKYNCTQUADLTIIDNIEEMNFLRYKCSSDHWG	94	
QY	135	L---RNNSGWRWDGEPNLRSLSNSFVOTCAINKNGLOASCEVPDLHGVCCK	186	
Dd	95	LKWAKRTGT-QWVDGA--TFTKFGMRGSRGGCAYLSDCGAATARCCTERKWI CRK	146	

FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,523
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0281 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>

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RESULT 14
US-10-424-599-222182
; Sequence 222182, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 222182
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(95)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4265C.1.pap
US-10-424-599-222182

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[illegible]

Tue Aug 10 17:15:48 2004

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127 SEAFQWIGLRNN---SGWRWEDGS 147
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64  SQAFFWIGIHNEERSXWLWEDGT  87

RESULT 15
US-09-944-807-6
; Sequence 6, Application US/09944807
; Patent NO. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-6

Query Match      16.4%; Score 168; DB 9; Length 149;
Best Local Similarity 31.3%; Pred. No. 3.8e-09;
Matches 36; Conservative 24; Mismatches 49; Indels 6; Gaps 3;

QY      75  CPDRWMKYGHCYYFSEVEEKDWNSSLEFCLARDSHLLVITDNOEMLLQVFLSEAFQWIG 134
Db      35  CPDWTGFGKCYFFKEEGDWNSSKXNCSTQHADLTIIDIEEMFLRYKCSSDHWIG 94

QY      135  L--RRNSGWRWEDGSPFNFSRISNSFVOTCGAINKNGLQASCEVPLHGVCCK 186
Db      95  LKWKAKNRTG--OWVHGA--TTTKSGFMWKGSGGCAYLSDGGAATARCYPETERKWI CRK 146

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Search completed: August 10, 2004, 16:40:34
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:32:44 ; Search time 18 Seconds
(without alignments)
542.073 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVIYSMLELPATQAQN.....GLQASSCEVPLHGVCKKVRLL 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 303294

Minimum DB seq length: 0

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525.5	51.4	188	3	US-08-722-126A-5
2	525.5	51.4	188	5	PCT-US95-04258-5
3	430	42.0	76	4	US-09-531-056A-23
4	370.5	36.2	114	3	US-08-722-126A-6
5	370.5	36.2	114	5	PCT-US95-04258-6
6	196.5	19.2	179	1	US-08-890-095-9
7	196.5	19.2	179	2	US-08-850-578-2
8	196.5	19.2	179	2	US-08-688-342-3
9	196.5	19.2	179	3	US-09-113-788-3
10	196.5	19.2	179	3	US-09-113-789-9
11	175.5	17.2	168	3	US-08-772-440-17
12	173	16.9	175	3	US-08-772-440-15
13	172	16.8	134	3	US-08-772-440-16
14	169.5	16.6	120	3	US-08-543-246B-18
15	169.5	16.6	135	3	US-08-543-246B-17
16	166	16.2	134	3	US-08-543-246B-20
17	164.5	16.1	135	3	US-08-543-246B-19
18	162	15.8	129	3	US-08-722-126A-10
19	162	15.8	129	5	PCT-US95-04258-10
20	161.5	15.8	173	4	US-09-531-056A-4
21	158.5	15.5	79	4	US-09-531-056A-19
22	158	15.4	176	3	US-08-772-440-8
23	158	15.4	180	3	US-08-772-440-31
24	156.5	15.3	77	4	US-09-531-056A-22
25	155.5	15.2	122	3	US-08-722-126A-9
26	155.5	15.2	122	5	PCT-US95-04258-9
27	155.5	15.2	187	4	US-09-127-946-12

28 155 15.2 115 3 US-08-722-126A-8
29 155 15.2 115 5 PCT-US95-04258-8
30 154 15.1 126 3 US-08-772-440-10
31 152 14.9 78 4 US-09-531-056A-15
32 152 14.9 78 4 US-09-531-056A-16
33 150 14.7 141 4 US-09-535-521-14
34 150 14.7 187 4 US-09-535-521-17
35 148 14.5 78 4 US-09-531-056A-20
36 147.5 14.4 139 4 US-09-535-521-11
37 147.5 14.4 174 2 US-08-401-530A-2
38 147.5 14.4 174 2 US-08-709-662-2
39 147.5 14.4 175 1 US-08-909-925-6
40 146.5 14.3 123 4 US-09-535-521-25
41 146 14.3 117 1 US-07-614-443A-2
42 146 14.3 117 1 US-08-294-859-2
43 146 14.3 117 1 US-08-481-676-2
44 142 13.9 77 4 US-09-531-056A-21
45 142 13.9 131 3 US-08-772-440-23

ALIGNMENTS

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-5

Query Match 51.4%; Score 525.5; DB 3; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;

Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTSVIVSMLELPATQAQNDYGPQOKSSSKPSCSLVAITGLITAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTVILMSLLYQRTL 60

Qy 61 CQGSNYSTCASCPSPDRWMMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
Db 61 CCGSKGFMCSQCRPNLWNRNGSHCYFVSMEKRDWNSSLKFCADKSGHLLTFFDNQGVN 120

Qy 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPNFSRISSNSFVQTCGAINKNGIQAASCEVPL 180
Db 121 LFQYVGEDFWIGLRDIDGWRWEDGPALSLS-ILNSVYQKCGTIHRCGLHASSCEVAL 179

Qy 181 HGVCKV 187
Db 180 QWICEKV 186

RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-5

Query Match 51.4%; Score 525.5; DB 5; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.1e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTSVIVSMLELPATQAQNDYGPQOKSSSKPSCSLVAITGLITAVLLSVLLYQWIL 60
Db 1 MADNSIYSTLELPAPRVQDDSRWKVAVLHRPCVSYLVMMVALGLLTVILMSLLYQRTL 60

Qy 61 CQGSNYSTCASCPSPDRWMMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMS 120
Db 61 CCGSKGFMCSQCRPNLWNRNGSHCYFVSMEKRDWNSSLKFCADKSGHLLTFFDNQGVN 120

Qy 121 LLQVFLSEAFWCWIGLRNNSGWRWEDGSPNFSRISSNSFVQTCGAINKNGIQAASCEVPL 180
Db 121 LFQYVGEDFWIGLRDIDGWRWEDGPALSLS-ILNSVYQKCGTIHRCGLHASSCEVAL 179

Qy 181 HGVCKV 187
Db 180 QWICEKV 186

RESULT 3
US-09-531-056A-23
; Sequence 23, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531.056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23

Query Match 42.0%; Score 430; DB 4; Length 76;
Best Local Similarity 98.7%; Pred. No. 6e-39; Indels 0; Gaps 0;
Matches 75; Conservative 0; Mismatches 1;

Qy 73 PSCDPRWMMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEAFCW 132
Db 1 PSCDPRWMMKYNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMSLLQVFLSEAFCW 60

Qy 133 IGLRNSGWRWEDGSP 148
Db 61 IGLRNSGWRWEDGSP 76

RESULT 4
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTHMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257

Query Match 36.2%; Score 370.5; DB 3; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32; Indels 1; Gaps 1;
Matches 66; Conservative 18; Mismatches 28;
QY 75 CPDRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLQLQVFLSEAFQWIG 134
DB 1 CPNLWNRNGSHCYFVSMEKRDWNSSLKFCADKGSLLTFPDNQGNLFOEYVGVDFYWG 60
QY 135 LRNSGWRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPLHGVCKV 187
DB 61 LRIDIDGWRWEDGPALSLS-ILSNSVYQKGTTHRCGLHASSCEVALQWICEKV 112

RESULT 5
PCT-US95-04258-6
; Sequence 6, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT: BROWDY, Roger L.
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-6

Query Match 36.2%; Score 370.5; DB 5; Length 114;
Best Local Similarity 58.4%; Pred. No. 2.6e-32; Indels 1; Gaps 1;
Matches 66; Conservative 18; Mismatches 28;
QY 75 CPDRMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQEMSLQLQVFLSEAFQWIG 134
DB 1 CPNLWNRNGSHCYFVSMEKRDWNSSLKFCADKGSLLTFPDNQGNLFOEYVGVDFYWG 60
QY 135 LRNSGWRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPLHGVCKV 187
DB 61 LRIDIDGWRWEDGPALSLS-ILSNSVYQKGTTHRCGLHASSCEVALQWICEKV 112

RESULT 6
US-08-690-095-9
; Sequence 9, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1098617
US-08-690-095-9

Query Match 19.2%; Score 196.5; DB 1; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
QY 35 CSCIVATILGLTAVLLSVLLVQWILCOGSN--YSTCASCPCSPDRMKYGNHCYFVSVE 92
DB 20 CLSLMA-TLIGLLKNSFTKLSTPEFTPGNTELOKSDCCQCKWGVYCNCFISSE 78
QY 93 EXDWNSSLEFCLARDSHLLVITDQEMSLQLQVFLSEAFQWIGL---RNSGWRWEDGSP 149
DB 79 QKTWNEHRLCASQKSSLLQLQNTDELDFMS--SSQOFYWGIGLSSEHTAWLWENGSA 136
QY 150 NFSRISNSF---VOTCGAINKNG-LQASSCEVPLHGVCKK 186
DB 137 --SQVLFPSFETFTNTKNCIAYNPNGNALDESCEDEKRNRYICKQ 176

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RESULT 7
US-08-650-578-2
; Sequence 2, Application US/08650578
; Patent No. 5811284
; GENERAL INFORMATION:
; APPLICANT: Chang, Chiwen
; APPLICANT: Aramburu Beltran, Jose
; APPLICANT: Lopez-Botet, Miguel
; APPLICANT: Phillips Jr., Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Purified Mammalian NK Antigens and
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,578
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,339
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin F.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-578-2

Query Match          19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCIVAITGLLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRWMKYGNHCYFSVE 92
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 20 CLSLMA-TLGILLKNSFTKLSIEPAFTPGNIELQKSDCCSCQEKWVGRCNCYFISSE 78
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 93 EKDNSSLEFLCARDSHLLVITDNQEMSLQLQVFLSEAFWCIGL---RNNSGRWEDGSP 149
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 79 QKTWNESRHLCAQSKSLLQLQNTDELDFMS--SSQOFYWIGLSYSEHTAWLWENGSA 136
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 150 NFRISNSNF-----VQTCGAINKNG-LQASSCEVPLHGVCCK 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 137 --SQYLPSPETNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8
US-08-688-342-3
; Sequence 3, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:

; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:

; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/113,788
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/688,342
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 179 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1098616
/
US-09-113-788-3
/
Query Match 19.2%; Score 196.5; DB 2; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
/
QY 35 CSCLVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRMVKYGNHCYFVSVE 92
Db 20 CLSLMA-TLIGLLKNSFTKLSIEPATPGNIELQKSDCCSQKWKVGRNCYFISSE 78
/
QY 93 EKDNSSLEFCLARDSHLIVITDNOEMSLLOVFLSEAFWIGL---RNNSGWRWEDGSPL 149
Db 79 QKTWNEHRLCASQKSLLOLQNTDLDLDFMS--SSQCFYWIGLSYEHTAWLWENGSA 136
/
QY 150 NFRSISSNF---VOTCGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLPSPFETNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
/
RESULT 10
US-09-113-789-9
/ Sequence 9, Application US/09113789
/ Patent No. 6034219
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Goli, Surya K.
/ TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/
COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/113,789
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/690,095
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/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0110 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 179 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 1098617
/
US-09-113-789-9
/
Query Match 19.2%; Score 196.5; DB 3; Length 179;
Best Local Similarity 32.7%; Pred. No. 2.4e-13;
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;
/
QY 35 CSCLVAITLGLTAVLLSVLLYQWILCOGSN--YSTCASCPCSPDRMVKYGNHCYFVSVE 92
Db 20 CLSLMA-TLIGLLKNSFTKLSIEPATPGNIELQKSDCCSQKWKVGRNCYFISSE 78
/
QY 93 EKDNSSLEFCLARDSHLIVITDNOEMSLLOVFLSEAFWIGL---RNNSGWRWEDGSPL 149
Db 79 QKTWNEHRLCASQKSLLOLQNTDLDLDFMS--SSQCFYWIGLSYEHTAWLWENGSA 136
/
QY 150 NFRSISSNF---VOTCGAINKNG-LQASSCEVPLHGVCCK 186
Db 137 --SQYLPSPFETNTKNCIAYNPNGNALDESCEDKNRYICKQ 176
/
RESULT 11
US-08-772-440-17
/ Sequence 17, Application US/08772440
/ Patent No. 6046158
/ GENERAL INFORMATION:
/ APPLICANT: Ariizumi, Kiyoshi
/ APPLICANT: Takashima, Akira
/ TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
/ TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES
/ TITLE OF INVENTION: THEREOF
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77210
/
COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/772,440
/ FILING DATE: CONCURRENTLY HERewith
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parker, David L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: UTMD:493
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512/418-3000
/ TELEFAX: 512/474-7577
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
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; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-17

Query Match
Best Local Similarity 17.2%; Score 175.5; DB 3; Length 168;
Matches 42; Conservative 28; Mismatches 51; Indels 27; Gaps 4;

QY 25 QOKSSSKPSCSLVAITGLTAVLLS-----VLLYQWILCOGS-----NYSTCA 70
Db 3 QERQSGKGVCTURLWLSAAVISMLLSTCFIASCVCVTYQFIMDQPSRRLYELHTYHSSL 62
QY 71 SCPS-----CPDRWKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOE 118
Db 63 TCFSEGTVMSEKMGCCNHNHWSFGSSCYLLSTKENFWSTSEQNCVQMGHLLVINTAE 122
QY 119 MSLLQVFLSEAFW-IGLRNNSGWRWED 145
Db 123 QNFITQQLNESLSYFLGLSNPKNKGWND 150

RESULT 12
US-08-772-440-15
; Sequence 15, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772 440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-15

Query Match
Best Local Similarity 16.9%; Score 173; DB 3; Length 175;
Matches 52; Conservative 34; Mismatches 64; Indels 38; Gaps 9;

QY 25 QOKSSSKPSCSLVAITGLTAVLLSLLYQWILCOGSNYSTC--ASCPS-----CPD 77
Db 3 QERQSGKGVCTURLWLSAAVISMLLSTCFIASCVCVTYQFIMDQPSRRLYELHTYHSSL 47

US-08-772-440-16
; Sequence 16, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772 440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-16

Query Match
Best Local Similarity 16.8%; Score 172; DB 3; Length 134;
Matches 42; Conservative 26; Mismatches 43; Indels 26; Gaps 6;

QY 25 QOKSSSKPSCSLVAITGLTAVLLSLLYQWILCOGSNYSTC--ASCPS-----CPD 77
Db 3 QERQSGKGVCTURLWLSAAVISMLLSTCFIASCVCVTYQFIMDQPSRRLYELHTYHSSL 47
QY 78 RWMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMLLQVFLSEAFW-IGL- 135
Db 48 HWSFGSSCYLLSTKENFWSTSEQNCVQMGHLLVINTAEQNFITQQLNESLSYFLGLS 107
QY 136 --RNNSGWRWEDGSPN-----FSRISNSFVQTCGAI-----NKGILQASCEVPLHGV 183
Db 108 DPQNGKQWIDDTFFSQNVRFWHPHPNLPPEERCVSIVYWNPSKMGWNDVFCDSKHNSI 167
QY 184 C--KKVRL 189
Db 168 CEMKKIYL 175

RESULT 13
US-08-772-440-16
; Sequence 16, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772 440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-16

Query Match
Best Local Similarity 16.8%; Score 172; DB 3; Length 134;
Matches 42; Conservative 26; Mismatches 43; Indels 26; Gaps 6;

QY 25 QOKSSSKPSCSLVAITGLTAVLLSLLYQWILCOGSNYSTC--ASCPS-----CPD 77
Db 3 QERQSGKGVCTURLWLSAAVISMLLSTCFIASCVCVTYQFIMDQPSRRLYELHTYHSSL 47
QY 78 RWMKYGNHCYFVSVEEKDWNSSLEFCLARDSHLLVITDNOEMLLQVFLSEAFW-IGL- 135
Db 48 HWSFGSSCYLLSTKENFWSTSEQNCVQMGHLLVINTAEQNFITQQLNESLSYFLGLS 107
QY 136 --RNNSGWRWEDGSPN-----FSRISNSFVQTCGAI-----NKGILQASCEVPLHGV 183
Db 108 DPQNGKQWIDDTFFSQNVRFWHPHPNLPPEERCVSIVYWNPSKMGWNDVFCDSKHNSI 167
QY 184 C--KKVRL 189
Db 168 CEMKKIYL 175

RESULT 14
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US-08-543-246B-18
; Sequence 18, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-543-246B-18
; Query Match 16.6%; Score 169.5; DB 3; Length 120;
; Best Local Similarity 31.6%; Pred. No. 1.1e-10;
; Matches 37; Conservative 20; Mismatches 55; Indels 5; Gaps 3;
QY 72 CPSCPRWKNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAF 131
Db 3 CGHCPEWITYNSCYIGKERTWESLLACTSKNSLLSIDNEEMKFLSIISPSS-- 60
QY 132 WIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVOTCGAINKNGLOASSCEVPLHGVC 185
Db 61 WIGVFRNSSHHPTWMTNGLAFLKHEIKDSNAELNCAVLQVNRKLSAQCGSSIIYHCK 117
RESULT 15
US-08-543-246B-17
; Sequence 17, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; natural killer cells

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; US-08-543-246B-17
; Query Match 16.6%; Score 169.5; DB 3; Length 135;
; Best Local Similarity 31.6%; Pred. No. 1.3e-10;
; Matches 37; Conservative 20; Mismatches 55; Indels 5; Gaps 3;
QY 72 CPSCPRWKNYHCYFVSVEEKDWNSSLEFCLARDSHLLVITDQMSLLQVFLSEAF 131
Db 18 CGHCPEWITYNSCYIGKERTWESLLACTSKNSLLSIDNEEMKFLSIISPSS-- 75
QY 132 WIGL-RNNSGWRWEDGSPLNFSR--ISSNSFVOTCGAINKNGLOASSCEVPLHGVC 185
Db 76 WIGVFRNSSHHPTWMTNGLAFLKHEIKDSNAELNCAVLQVNRKLSAQCGSSIIYHCK 132
Search completed: August 10, 2004, 16:35:49
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:39:40 ; Search time 13.5 Seconds

(without alignments)
1339.556 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSIYSTLELPEAPQVOD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 95185

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	838	81.4	188	2 I59421	mast cell function
2	163.5	15.9	146	2 JC7135	agkisacutacin beta
3	155.5	15.1	156	2 T28141	C type lectin, B 1
4	152.5	14.8	146	2 JC4691	coagulation factor
5	146.5	14.2	146	2 JC7105	aggreitin beta chai
6	138	13.4	167	1 WMVZF2	hepatic lectin hom
7	136.5	13.3	170	2 T28140	natural killer cel
8	135	13.1	144	2 PC7027	aggreitin alpha cha
9	119	11.6	133	2 A47267	botrocetin alpha c
10	117.5	11.4	123	2 B42972	coagulation factor
11	114.5	11.1	152	2 JC7134	agkisacutacin alph
12	113.5	11.0	125	2 B47267	botrocetin beta ch
13	109.5	10.6	155	2 S78774	perlucin - Haloti
14	107.5	10.4	116	1 WMVZF8	hepatic lectin hom
15	105.5	10.3	125	2 JC5059	bitiscetin beta ch
16	104	10.1	152	2 JC4690	coagulation factor
17	103	10.0	175	2 S29822	pancreatitits-assoc
18	102.5	10.0	162	1 LNR3	lectin BRAJ-2 prec
19	101.5	9.9	123	2 JC2415	echicetin beta cha
20	101.5	9.9	162	1 LNR31	lectin BRAJ-1 prec
21	101	9.8	175	2 A49616	pancreatitits-assoc
22	97.5	9.5	165	2 A28351	pancreatit stone p
23	97	9.4	135	2 A38609	lectin, galactose-
24	95	9.2	174	2 S54979	pancreatitits-assoc
25	94	9.1	175	2 A41719	pancreatit stone p
26	93	9.0	163	1 A43413	antifreeze protein
27	91	8.8	129	2 JC4329	coagulation factor
28	90.5	8.8	166	2 A45751	pancreatit stone p
29	90	8.7	131	2 JC5058	bitiscetin alpha c

30	90	8.7	166	1 RGHULA	regenerating islet
31	89.5	8.7	166	1 RGHULB	regenerating islet
32	86	8.4	174	2 I83377	regenerating prote
33	86	8.4	175	2 A37194	pancreatic thread
34	85	8.3	40	2 S56007	tokaracetin beta c
35	81.5	7.9	143	1 WMVZEL	hepatic lectin hom
36	81	7.9	165	2 A47148	reg I, regeneratin
37	80.5	7.8	142	2 S78596	ovocleidin - chick
38	79	7.7	40	2 B56829	alboaggregin-B alp
39	79	7.7	140	2 JC7786	lectin CEL-I, N-ac
40	78	7.6	174	1 A48689	pancreatitits-assoc
41	77.5	7.5	173	2 S10548	lectin - barnacle
42	76	7.4	159	2 T30745	hypothetical prote
43	75.5	7.3	147	2 A36697	echinoidin - sea u
44	75	7.3	166	2 T28809	hypothetical prote
45	75	7.3	173	2 B47148	reg II, regenerati

ALIGNMENTS

RESULT 1

I59421

mast cell function associated antigen - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I59421

R:Guthmann, M.D.; Tal, M.; Pecht, I.

Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995

A:Title: A secretion inhibitory signal transduction molecule on mast cells is another C

A:Reference number: I59421; MUID:96016176; PMID:7568140

A:Accession: I59421

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-188 <RES>

A:Cross-references: EMBL:X79812; NID:gi020141; PIDN:CAA56208.1; PID:gi020142

C:Genetics:

A:Gene: mafa

Query Match 81.4%; Score 838; DB 2; Length 188;
Best Local Similarity 80.7%; Pred. No. 1.3e-74;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSIYSTLELPEAPQVODSRWKLKAVLHHRPHLSRFAMVALGLLTIVLSLLMYQRTIL 60

Db 1 MADSSIYSTLELPEAPRVQDDSRWKKVAVLRPCVSYLVWVALGLLTIVLSLLMYQRTIL 60

QY 61 CCGSKDSTCSHCPCSPCILLWTRNGSHCYFYSMEKKDWNSSLKFCADKSGSHLLTPPDNQGVK 120

Db 61 CCGSKGFCMSQSRCPENLWNRNGSHCYFYSMEKKDWNSSLKFCADKSGSHLLTPPDNQGVN 120

QY 121 LFEYGLQDFYWGILNRIDGWEGGPAALSILNTSLIQRCAIHRNGIQASSCEVALQ 180

Db 121 LFEQYVGDFYWGILNRIDGWREDGPAALSILNSVYVQKGTIHRCGIHASSCEVALQ 180

QY 181 WICKKVL 187

Db 181 WICEKVL 187

RESULT 2

JC7135

agkisacutacin beta chain precursor - sharp-nosed viper

N:Alternate names: fibrinogenolytic venom protein

C:Species: Agkistrodon acutus (sharp-nosed viper)

C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000

C:Accession: JC7135; PC7038

R:Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

Biochem. Biophys. Res. Commun. 265, 530-535, 1999

A:Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom

A:Reference number: JC7134; MUID:20025379; PMID:10558903

A:Accession: JC7135

A:Molecule type: mRNA

A;Residues: 1-146 <CHE>
A;Cross-references: GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50:59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkiscutacin beta chain #status experimental <MAT>

Query Match 15.9%; Score 163.5; DB 2; Length 146;
Best Local Similarity 30.2%; Pred. No. 1e-08;
Matches 48; Conservative 15; Mismatches 71; Indels 25; Gaps 6;

QY 35 LSRFAMVALGLTIVILMSLLMYQILCCGSKDSTCSHCPCPIILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLLLVVFL-----SLSGTAADCPs-----EWSYEGHCYKPFDEPK 44

QY 95 DWNSSLKFCAD--KGSHLLTFPDNQG---VKLFGEYLGQDFYWIGLRNI-DG--WRWEG 145
Db 45 TWADAERFCTQHKGSHLAFHSSEADFVVTLTPTSLKTLVWIGLKNIWNGCYWKNWD 104

QY 146 GPALSLRLITNSLQRCGALHNRGLQASSCEVALQWICK 184
Db 105 GTKLDYKDWRQEFCECLSRVTNNWLSMDCGTTCFVCK 143

RESULT 3
T28141
C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28141
R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: Z20475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-156 <ML>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAAL8961.1
A;Experimental source: clone c812
C;Genetics:
A;Gene: Blec
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Query Match 15.1%; Score 155.5; DB 2; Length 156;
Best Local Similarity 25.0%; Pred. No. 6.7e-08;
Matches 39; Conservative 24; Mismatches 68; Indels 25; Gaps 6;

QY 39 AMVALGLTIVILMSLLMYQILCCGSKDSTCSH---CPCPIILWTRNGSHCYFYSMEKKD 95
Db 3 AVFTVLLITAVAFVAQFQ-----PHQPQCAQCFDWMIGPRGKCYFSEDSN 50

QY 96 WNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNI-DG---WRWEGPALs- 150
Db 51 WTSQNNCSALGASLAFDSAEGLSFTMRHKGSSPHWGLSR-EGKEHPWENRSPLSH 109

QY 151 -LRILNLSLQRCGALHNRGLQASSCEVALQWICK 185
Db 110 LFOVQGDGL---CAYLDAGLSGSHCSGTRRNWVCTK 142

RESULT 4
JC4691
coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4691; B39332; JC4330
R;Matsuzaki, R.; Yoshihara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from
A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4691
A;Molecule type: mRNA
A;Residues: 1-146 <MAT1>
A;Cross-references: DDBJ:D83332; NID:g1402641; PIDN:BAA11888.1; PID:g1402642
A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolated
a tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
A;Accession: B39332
A;Molecule type: protein
A;Residues: 24-146 <AT0>
R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav
A;Reference number: JC4329; MUID:96318509; PMID:8749314
A;Accession: JC4330
A;Molecule type: protein
A;Residues: 24-146 <AT2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; lectin; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: factor IX/X binding protein chain B #status predicted <MAT>
F;25-142/Domain: C-type lectin homology <ICH>
F;25-36;53-142;119-134/Disulfide bonds: #status predicted

Query Match 14.8%; Score 152.5; DB 2; Length 146;
Best Local Similarity 24.5%; Pred. No. 1.2e-07;
Matches 39; Conservative 25; Mismatches 70; Indels 25; Gaps 5;

QY 35 LSRFAMVALGLTIVILMSLLMYQILCCGSKDSTCSHCPCPIILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLLLVVFL-----SLSGTAADCPD---WSSYEGHCYKPFSEPK 44

QY 95 DWNSSLKFCADK--GSHLLTFPDNQG---VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
Db 45 NWADAENFCTQKHAGHLSVFSQSEADFVVKLAFQTFGHSIFWMLGSLNVMQCNQWSN 104

QY 146 GPALSLRLITNSLQRCGALHNRGLQASSCEVALQWICK 184
Db 105 AAMLYKAWAESYCYFYSKSTNNKWSRACRMMAQFVCE 143

RESULT 5
JC7105
aggritin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: JC7105
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggritin, a collagen-like platelet
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: JC7105
A;Molecule type: mRNA
A;Residues: 1-146 <CHU>
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom

Query Match 14.2%; Score 146.5; DB 2; Length 146;
Best Local Similarity 29.0%; Pred. No. 4.7e-07;
Matches 47; Conservative 18; Mismatches 66; Indels 31; Gaps 8;

QY 35 LSRFAMVALGLTIVILMSLLMYQILCCGSKDSTCSHCPCPIILWTRNGSHCYFYSMEKK 94
Db 1 MGRFIFVSGLLLVVFL-----SLSGTADCPG---WSSYEGHCYKPFNEPK 44

QY 95 DWNSSLKFC--ADKSGHLLTFPDNQG---VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145

Db 45 NWADAEKFKLQPKSHLSVFSQAEDAFVVKLTRPLKANLWVWGLSNLWEGCNQWSD 104
QY 146 GFALSLRLITNSLIQRCGA---IHRNGLQASSCEVALQWICK 184
Db 105 GARLNYKDWQEQ--SECLAFRGVHTWLN-MDCSSCSFVCK 143

RESULT 6
WVZF2
hepatitis B virus (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])
C:Species: fowlpox virus
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C:Accession: B29963
R:Tomley, F.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A>Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox virus
A:Reference number: J0442; MUID:88229622; PMID:2836548
A:Accession: B29963
A:Molecule type: DNA
A:Residues: 1-167 <TOM>
A:Cross-references: GB:D00295; NID:g221380; PIDN:BAA00192.1; PID:g221383
C:Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homolog
C:Keywords: early protein
F:49-152/Domain: C-type lectin homolog <LCH>

Query Match 13.4%; Score 138; DB 1; Length 167;
Best Local Similarity 27.4%; Pred. No. 3.7e-06;
Matches 38; Conservative 28; Mismatches 62; Indels 12; Gaps 4;

QY 35 LSRFAMVALGLLVILMSLIMYQRIILCCGSKDSCCHPCSPILWTRNGSHCYFVSMEKK 94
Db 12 VSCYALTIVLIGLILFTILV---VVTCKWYAFYFVSFVPCDDEWIGYNSKCYFTINET 68
QY 95 DNMSLKFCDKSHLLTPPDNQGVKLFGEYLGQDFYWGIL---RNIDGWRW-----EGG 146
Db 69 NWDSKLCVDMSSLRIFNFIETLNFVSRY-GKGSWIDINQNRKIPGINSFYVEQGV 127
QY 147 PALSRLITNSLIQRCGAH 166
Db 128 NDICLLFDTSNIEMSCIFH 147

RESULT 7
T28140
natural killer cell receptor homolog - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T28140
R:Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A:Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A:Reference number: Z20475
A:Accession: T28140
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-170 <ML>
A:Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CRA18960.1
A:Experimental source: clone cb12
C:Genetics:
A:Gene: B-NK
A:Map position: 16
A>Note: Intron positions not resolved (incomplete sequence)

Query Match 13.3%; Score 136.5; DB 2; Length 170;
Best Local Similarity 25.6%; Pred. No. 5.3e-06;
Matches 31; Conservative 16; Mismatches 63; Indels 11; Gaps 3;

QY 72 CPSCPIILWTRNGSHCYFVSMEKKDWNSSLKFCADKSGHLLTFPDNQGVKLFGEYLGQDFY 131
Db 47 CLLCPQWRLIGDRCYELSTEGKGNWTQAKMKCNLQSLAVLRKKABEDHLQQMAGAEPV 106
QY 132 WIGLR-NIDGWRWGGGAL-----SLRLITNSLIQRCGAHNRNGLQASSCEVALQWICK 184

Db 107 WIGLEVSTNQKWKVDNSSNSTESDNLVWEN----RCGTFKNTKYEGDVCSGEHQWVCQ 162
QY 185 K 185
Db 163 K 163

RESULT 8
PC7027
aggreitin alpha chain - Malayan pit viper (fragment)
C:Species: Calloselasma rhodostoma (Malayan pit viper)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: PC7027
R:Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A>Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like platelet alpha chain
A:Reference number: PC7027; MUID:99443731; PMID:10512747
A:Accession: PC7027
A:Molecule type: mRNA
A:Residues: 1-144 <CHU>
A:Experimental source: venom gland
C:Superfamily: tetranectin; C-type lectin homolog
C:Keywords: disulfide bond; platelet aggregation; venom

Query Match 13.1%; Score 135; DB 2; Length 144;
Best Local Similarity 25.5%; Pred. No. 6.3e-06;
Matches 36; Conservative 23; Mismatches 64; Indels 18; Gaps 5;

QY 66 DSTSCHPCSPILWTRNGSHCYFVSMEKKDWNSSLKFC--ADKSGHLLTFPDNQGVKLF 123
Db 4 EGTRAGLEDCDFGWSFYDQHCYQAFNEQKTWDEAEFCRAQENGHAHLASIESNGEADFVS 63
QY 124 -----EYLQDPFYWIGLRNID-----GWRWEGGPALSLRLITNSLIQRCGAH-NGL 170
Db 64 WLISQKDELADEYVWIGLRAQNKQEQCSSEWSDGSSVYENLIDLHTKCGALEKLTGF 123
QY 171 QA---SSCEVALQWICKVLY 188
Db 124 RKWNYCYEQMFAFVCKLLFY 144

RESULT 9
A47267
botrocetin alpha chain - jararaca
N:Alternate names: two chain botrocetin alpha chain
C:Species: Bothrops jararaca (jararaca)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C:Accession: A47267; B37958
R:Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A>Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator protein
A:Reference number: A47267; MUID:93157385; PMID:8430107
A:Accession: A47267
A:Molecule type: protein
A:Residues: 1-133 <USA>
A:Experimental source: venom
A>Note: sequence extracted from NCBI backbone (NCBIP:124085)
R:Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sugita, T.
Biochemistry 30, 1957-1964, 1991
A>Title: Isolation and chemical characterization of two structurally and functionally different botrocetins
A:Reference number: A37958; MUID:91129280; PMID:1993206
A:Accession: B37958
A:Molecule type: protein
A:Residues: 1-40 <FUJ>
C:Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C:Superfamily: tetranectin; C-type lectin homolog
C:Keywords: hemagglutinin; heterodimer; venom
F:2-128/Domain: C-type lectin homolog <LCH>
F:2-13,30-128,103-120/disulfide bonds: #status experimental
F:80/Disulfide bonds: interchain (to beta-75) #status experimental

Query Match 11.6%; Score 119; DB 2; Length 133;

```

Best Local Similarity 25.4%; Pred. No. 0.00021;
Matches 29; Conservative 26; Mismatches 33; Indels 26; Gaps 7;

QY 75 CPILWTRNGSHCYFMSMEKKDWNSSLKFCAD--KGSHLLTFPDNGVKLFG---EYLG-- 127
DB 2 CPDSSVEGNCYKFFQKMMWADAEFCBQAKGHLVS-----IKIYSKEKDFVGD 55

QY 128 -----QDFY-WIGLR--NID--GWWEVGGPALSRLITNSLIQRCGAH 168
DB 56 VTKNIQSSDLXAWIGLRVYENKEKQCSSESDGSSVSVENVETVKKCFAL 109

RESULT 10
B42972
coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C;Species: Viper russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: B42972
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
J. Biol. Chem. 267, 14109-14117, 1992
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no
A;Reference number: A42972; MUID:92332516; PMID:1629211
A;Contents: V. x. siamensis
A;Accession: B42972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <TAK>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:108408)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;4-121/Domain: C-type lectin homology <LCH>
F;4-15,32-121,98-113/Disulfide bonds: #status predicted

Query Match 11.4%; Score 117.5; DB 2; Length 123;
Best Local Similarity 26.4%; Pred. No. 0.00027;
Matches 32; Conservative 15; Mismatches 61; Indels 13; Gaps 4;

QY 75 CPILWTRNGSHCYFMSMEKKDWNSSLKFCAD--KGSHLLTFPDNGQ---VKLFGEYLQ 128
DB 4 CPDSSVEGNCYKFFQKMMWADAEFCBQAKGHLVS-----IKIYSKEKDFVGD 53

QY 129 DFVWIGLRNIDGWR-----MEGGPALSRLITNSLIQRCGAHNGIQASCEVALOWIC 183
DB 64 PATWIGLGNM--WKDCRMENSDRGVVKYKALAEESYCLIMITHEKEWKSMTCNFIAPVVC 121

QY 184 K 184
DB 122 K 122

RESULT 11
JC7134
agkisacutacin alpha chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenolytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7134; PC7037
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7134
A;Molecule type: mRNA
A;Residues: 1-152 <CHE>
A;Cross-references: GB:AF176420
A;Experimental source: venom gland
A;Accession: PC7037
A;Molecule type: protein
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>

```

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F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>

Query Match 11.1%; Score 114.5; DB 2; Length 152;
Best Local Similarity 23.6%; Pred. No. 0.00067;
Matches 35; Conservative 18; Mismatches 60; Indels 35; Gaps 6;

QY 35 LSRFAMVALGLTILVLSLLMYQRIICGSKDSTCSHCPCPILWTRNGSHCYFMSMEKK 94
DB 1 MGRFIFVSFGLLVVFL-----SLSGTAADCSG---WSSVEGHCYKVPKQSK 44

QY 95 DWNSSLKFCADK--GSHLLTFPDNGVKLFGYEQDF-----YWIGLR-----NI 138
DB 45 TWADAESFCTKQVNGGHLVSISSGEADFAHLIAQIKSAKIHWIGLRAQNKKEKQCSI 104

QY 139 DGWWEVGGPALSRLITNSLIQRCGAH 166
DB 105 E---WSDGSSISVENWIEESKKCLGVH 129

RESULT 12
B47267
botrocetin beta chain - jararaca
N;Alternate names: two chain botrocetin beta chain
C;Species: Bothrops jararaca (Jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: B47267; C37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator p
A;Reference number: A47267; MUID:93157385; PMID:8430107
A;Accession: B47267
A;Molecule type: protein
A;Residues: 1-125 <USA>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:124086)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Su
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally
A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: C37958
A;Molecule type: protein
A;Residues: 1-40 <FU>
C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 11.0%; Score 113.5; DB 2; Length 125;
Best Local Similarity 31.3%; Pred. No. 0.00069;
Matches 26; Conservative 12; Mismatches 32; Indels 13; Gaps 4;

QY 75 CPILWTRNGSHCYFMSMEKKDWNSSLKFCADK--GSHLLTFPDNGQV----KLFGEYLQ 128
DB 2 CPDSSVEGHCYKFFQKMMWADAEFCBQAKGHLVS-----IKIYSKEKDFVGD 61

QY 129 DFVWIGLRNIDGW-----RWEGG 146
DB 62 DVVWIGLSDV--WNKCRFEWTDG 82

RESULT 13
S78774
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C;Species: Haliotis laevigata
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
C;Accession: S78774
R;Mann, K.
submitted to the Protein Sequence Database, January 2000
A;Reference number: S78774
A;Contents: S78774
A;Accession: S78774

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